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OM protein - protein search, using sw model

Run on: June 1, 2003, 17:29:01 ; Search time 824 Seconds
(without alignments)
650.993 Million cell updates/sec

Title: US-09-634-252A-4
Perfect score: 4553
Sequence: 1 MKPPSSSRQPLAGCSLAG.....GMGFKVKKRRDPYQCGP

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA Main
1: /cgnt2_6/ptodata/1/paa/PCNUS_COMB.pep.*
2: /cgnt2_6/ptodata/1/paa/US06_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID
1	4553	100.0	832	20 US-09-634-252A-4
2	4553	100.0	832	21 US-09-791-537-64795
3	4553	100.0	832	22 US-09-824-129-3
4	4553	100.0	832	26 US-10-202-675-4
5	4259.5	93.6	829	21 US-09-791-537-142799
6	4186	91.9	776	21 US-09-760-484-315

Description

Sequence 4, Appl 1
Sequence 4, Appl 1
Sequence 4, Appl 1
Sequence 4, Appl 1
Sequence 4, Appl 1
Sequence 315, App

7	3851	84.6	709	20	US-09-631-534-10	Sequence 10, Appl
8	3851	84.6	709	26	US-10-260-506-10	Sequence 10, Appl
9	3621	79.5	696	20	US-09-631-534-2	Sequence 2, Appl
10	3621	79.5	696	22	US-09-809-617-2	Sequence 2, Appl
11	3621	79.5	696	22	US-09-809-790-2	Sequence 2, Appl
12	3621	79.5	696	26	US-10-260-506-2	Sequence 2, Appl
13	2295	50.4	513	27	US-60-212-656-285	Sequence 285, App
14	2295	50.4	513	27	US-60-230-435-1146	Sequence 1146, Ap
15	2027	44.5	773	21	US-09-791-537-137203	Sequence 137203,
16	1985.5	43.6	870	21	US-09-791-537-85165	Sequence 85165, A
17	1985	43.6	867	20	US-09-634-252A-6	Sequence 6, Appl
18	1985	43.6	867	21	US-09-791-537-38234	Sequence 38234, A
19	1985	43.6	867	26	US-10-202-675-6	Sequence 6, Appl
20	1983.5	43.6	823	21	US-09-791-537-107317	Sequence 107317,
21	1983.5	43.6	859	21	US-09-791-537-74496	Sequence 74496, A
22	1983	43.6	769	21	US-09-791-537-137085	Sequence 137085,
23	1971	43.3	821	21	US-09-791-537-79207	Sequence 79207, A
24	1971	43.3	857	21	US-09-791-537-79205	Sequence 79205, A
25	1960	43.0	785	27	US-60-212-656-502	Sequence 502, App
26	1960	43.0	785	27	US-60-230-435-1310	Sequence 1310, Ap
27	1960	43.0	808	27	US-60-207-315-352	Sequence 352, App
28	1958	43.0	858	27	US-60-212-656-480	Sequence 480, App
29	1958	43.0	858	27	US-60-230-435-1465	Sequence 1465, Ap
30	1868.5	41.0	664	21	US-09-791-537-107561	Sequence 107561,
31	1831	40.2	664	27	US-60-230-435-1070	Sequence 1070, Ap
32	1747.5	38.4	368	21	US-09-760-484-477	Sequence 477, App
33	1747.5	38.4	368	26	US-10-211-364-1048	Sequence 1048, Ap
34	1747.5	38.4	368	26	US-10-216-893-286	Sequence 286, App
35	1747.5	38.4	368	26	US-10-217-651-431	Sequence 431, App
36	1680	36.9	540	21	US-09-792-200B-18	Sequence 18, Appl
37	1680	36.9	540	21	US-09-792-200C-18	Sequence 18, Appl
38	1453	31.9	452	21	US-09-791-537-63648	Sequence 63648, A
39	1298	28.5	518	21	US-09-791-537-19102	Sequence 19102, A
40	1297	28.5	524	21	US-60-207-315-88445	Sequence 88445, A
41	1166.5	25.6	625	27	US-60-207-315-333	Sequence 333, App
42	1007.5	22.1	778	1	PCT-US00-14308-16	Sequence 16, Appl
43	1007.5	22.1	778	21	US-09-712-907-16	Sequence 16, Appl
44	1007.5	22.1	778	21	US-09-712-907A-16	Sequence 16, Appl
45	1007.5	22.1	778	23	US-09-955-504-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-634-252A-4
Sequence 4, Application US/09634252A
GENERAL INFORMATION:
APPLICANT: Cellecti, Douglas P.
TITLE OF INVENTION: SVPH3-13 AND SVPH3-17 DNA AND POLYPEPTIDES
FILE REFERENCE: 03260 0051-00304
CURRENT APPLICATION NUMBER: US/09/634, 252A
CURRENT FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/7074, 310
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 4
LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
US-09-634-252A-4

Query Match 100.0% Score 4553; DB 20; Length 832;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MKPPSSSRQPLAGCSLAGSGPGRGASVPASAPARTPCRLTLVLLPLPAAS	60
Db	1	MKPPSSSRQPLAGCSLAGSGCPGRGASVPASAPARTPCRLTLVLLPLPAAS	60
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61 RPRMGAAPSAPHMNETAEKNLGLVLADEDNLTLOONSSNISYSNAMOKEITLPSRLIY 120
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Db 121 INDESESPYHVLDTKARHOKHKNKAVHLAASFOIEAFSGFTLIDLINNGLLSSDYVEI 180
QY 181 HYENKPOYSKGEHCYHGSIRGVDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDE 240
Db 181 HYENKPOYSKGEHCYHGSIRGVDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDE 240
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Db 481 RDLFLOGGGACLFNRPTKLEPTECGNGYVEAGEEDCGFHVCEYGLCKKCSLSNGAHC 540
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QY 601 NGECSTRDNOCYIMGTAKAAGSDKFCYEKLNTEGTEKNGCKDGRWIOCSKHDFVCGFL 660
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Db 661 LCTNLTFRAPRIGOLOEIIPTSFYHOGRYIDCSGAHVVLDDDDTVGYVEDGTPCGPSMNC 720
QY 721 LDRKCLQIOALNMSSCPIDSKGKVCSGHGVCSNEATCICDFTWAGTDCSIRDPVRNLHP 780
Db 721 LDRKCLQIOALNMSSCPIDSKGKVCSGHGVCSNEATCICDFTWAGTDCSIRDPVRNLHP 780
QY 781 KDEGPKGSATNLIGISGAILVAIVLGGTGMGFKVKKRRRDPDQOGPI 832
Db 781 KDEGPKGSATNLIGISGAILVAIVLGGTGMGFKVKKRRRDPDQOGPI 832

RESULT 2
US-09-791-537-64795
; Sequence 64795, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64795
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-64795

Query Match 100.0%; Score 4553; DB 21; Length 832;
Best Local Similarity 100.0%; Pred. No. 0;

too like

Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKPGSSSRQPLAGCSLAGASCGPGRGASVPASAPARTPCORILLVLLPLAASS 60
Db 1 MKPGSSSRQPLAGCSLAGASCGPGRGASVPASAPARTPCORILLVLLPLAASS 60
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Db 181 HYENKPOYSKGEHCYHGSIRGVDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDE 240
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Db 241 KSTGRPHIIOKTLAGQYSKOMKNTLMERGDMFELSELQMLKRRKRAVNSRGIFPEEMKY 300
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Db 301 LELMIVNDHKTYYKRRSSHAHTNNFAKSVNLVDSIYKQOLNTRVYLVAETWTEKQID 360
QY 361 ITTNPVOMLHEFSKYRQRIKOHADAVHLISRVTFFHRRSSLSYFGVCSRTGCVNVEYG 420
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Db 421 LPMVAOVLQSLSLAQNLGIOMEPSSRRPKCDCTESMGCCIMEETGVSHSRKFSKSTLEY 480
QY 481 RDLFLOGGGACLFNRPTKLEPTECGNGYVEAGEEDCGFHVCEYGLCKKCSLSNGAHC 540
Db 481 RDLFLOGGGACLFNRPTKLEPTECGNGYVEAGEEDCGFHVCEYGLCKKCSLSNGAHC 540
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Db 601 NGECSTRDNOCYIMGTAKAAGSDKFCYEKLNTEGTEKNGCKDGRWIOCSKHDFVCGFL 660
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Db 781 KDEGPKGSATNLIGISGAILVAIVLGGTGMGFKVKKRRRDPDQOGPI 832

RESULT 3
US-09-824-129-3
; Sequence 3, Application US/09824129
; GENERAL INFORMATION:
; APPLICANT: Lopez-Olin, Carlos
; APPLICANT: Miguel, Santiago Cal
; APPLICANT: Freije, Jose Maria Perez
; APPLICANT: Garcia, Jose Manuel Perez
; APPLICANT: Bianchi, Albert Bernard
; APPLICANT: Trall, Pamela
; TITLE OF INVENTION: Methods and Compositions for Modulating
; FILE REFERENCE: D0015-NP
; CURRENT APPLICATION NUMBER: US/09/824,129

CURRENT FILING DATE: 2001-04-02
 PRIOR APPLICATION NUMBER: 60/194,164
 PRIOR FILING DATE: 2000-04-03
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 832
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-624-129-3

Query Match 100.0% Score 4553; DB 22; Length 832;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-202-675-4
 Sequence 4, Application us/10202675
 GENERAL INFORMATION:
 APPLICANT: Cerretti, Douglas P.
 TITLE OF INVENTION: SVPH-13 AND SVPH-17 DNA AND POLYPEPTIDES
 FILE REFERENCE: 03260,0051-00304
 CURRENT APPLICATION NUMBER: US/10/202,675
 CURRENT FILING DATE: 2002-07-23
 PRIOR APPLICATION NUMBER: US/09/634,252
 PRIOR FILING DATE: 2000-08-07
 PRIOR APPLICATION NUMBER: 60/074,310
 PRIOR FILING DATE: 1998-02-11
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 4
 LENGTH: 832
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-202-675-4

Query Match 100.0% Score 4553; DB 26; Length 832;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 MKPPSSSRPPPLAGCSLAGASCGPORGAGSVASAPARTPPCRLLVLLPPLAAS 60
 1 MKPPSSSRPPPLAGCSLAGASCGPORGAGSVASAPARTPPCRLLVLLPPLAAS 60
 61 RPRAGGAAPASAPHNNTAEKRLGLADEDNLTLOONSSNISYSNAMOKEITLPSRLIY 120
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 421 LPMVAQVLSQSLAONLGIOWEPSSRRPKCDCTESMGCIIMEETGVSHSRKFSKSILEY 480
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 481 RDLFLOGGGACLFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCKKCSLSNGAHC 540
 481 RDLFLOGGGACLFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCKKCSLSNGAHC 540
 541 SDGPCCNTNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCPNHLKHODGYACNOGRCY 600
 541 SDGPCCNTNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCPNHLKHODGYACNOGRCY 600
 541 SDGPCCNTNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCPNHLKHODGYACNOGRCY 600
 601 NGECKTRDNOCQYIWTGKAAGSDKFCYEKLTETEGKNGCGKGDGMWIOCSKHDFVCGFL 660
 601 NGECKTRDNOCQYIWTGKAAGSDKFCYEKLTETEGKNGCGKGDGMWIOCSKHDFVCGFL 660
 601 NGECKTRDNOCQYIWTGKAAGSDKFCYEKLTETEGKNGCGKGDGMWIOCSKHDFVCGFL 660
 661 LCTNLTRAPRIIGOLOGEITPTSFYHOGRAVSDCAHVAVLDDDDTVGVEDGTPCGPSMNC 720
 661 LCTNLTRAPRIIGOLOGEITPTSFYHOGRAVSDCAHVAVLDDDDTVGVEDGTPCGPSMNC 720
 661 LCTNLTRAPRIIGOLOGEITPTSFYHOGRAVSDCAHVAVLDDDDTVGVEDGTPCGPSMNC 720
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780

Db 721 LDRKLOIALNMSCPLDSKGVCSGHCNEATCICDPTWAGTDCSIDPVRNLHP 780
 Qy 761 KDEGPKGSATNLIGSIAGAILVAALVIGGTGKGFKNVKKRRPDPQGP 832
 Db 761 KDEGPKGSATNLIGSIAGAILVAALVIGGTGKGFKNVKKRRPDPQGP 832

RESULT 5

US-09-791-537-142799
 : Sequence 142799, Application US/09791537
 : GENERAL INFORMATION:
 : APPLICANT: Bionomix, Inc.
 : APPLICANT: Debe, Derek
 : APPLICANT: Danzer, Joseph
 : TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 : TITLE OF INVENTION: METHODS OF USE THEREOF
 : FILE REFERENCE: 261/210
 : CURRENT APPLICATION NUMBER: US/09/791,537
 : CURRENT FILING DATE: 2001-02-22
 : NUMBER OF SEQ ID NOS: 153055
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 142799
 : LENGTH: 829
 : TYPE: PRT
 : ORGANISM: Mus musculus
 : US-09-791-537-142799

Query Match 93.6%; Score 4239.5; DB 21; Length 829;
 Best Local Similarity 93.8%; Pred. No. 0;
 Matches 781; Conservative 16; Mismatches 31; Indels 5; Gaps 2;

Qy 1 MKPSSSSRPPPLACSLAGACGQPGRPAGSAPASAPAPRPPRLVLLPLLAASS 60
 Db 1 MKPSSISRPPLTGCSPGASCGRCPAPV-----PARAPCRLVLLPLPALATSS 56
 Qy 61 RPRAGGAAPAPPHNNTAEKNLGVLADEDTLQONSS-NISYSNAOKEITLPSRLIY 119
 Db 57 RPRAGGAAPAPPHNNTAEKNLGVLADEDTLQONSSNISYSNAOKEITLPSRLIY 116
 Qy 120 YINDSESPYHVLDTKARHQQHNKAVHLAQSFOIAFSGKFTLDLILNGLSSDY 179
 Db 117 YINDSESPYHVLDTKARHQQHNKAVHLAQSFOIAFSGKFTLDLILNGLSSDY 176
 Qy 180 IYENGKPOYSKGEHCYHGSINGVDSKVALSTCGLHGFEDDTFYVMIPELTD 239
 Db 177 IYHEDGOMTSKGEHCYHGSINGVDSKVALSTCGLHGFEDDTFYVMIPELTD 236
 Qy 240 EKSTGRPHIIQKTLAGOYSKOMNLTWERGDOMPELSELOMLKRRRAVNPSCGIFE 299
 Db 237 EKSTGRPHIIQKTLAGOYSKOMNLTWERGDOMPELSELOMLKRRRAVNPSCGIFE 296
 Qy 300 YLELMTVNDHKTYKKHRSHTNNFAKSVNLDVSIYEQLNTRVLAVAETWTEKDI 359
 Db 297 YLELMTVNDHKTYKKHRSHTNNFAKSVNLDVSIYEQLNTRVLAVAETWTEKDI 356
 Qy 360 DITTNPVOMLHEFSKYRQRIKOHADAIVHLISRTFYKRSLSYTGVCSTRGVNEY 419
 Db 357 DITTNPVOMLHEFSKYRQRIKOHADAIVHLISRTFYKRSLSYTGVCSTRGVNEY 416
 Qy 420 GLPMAVAOVLSSLOANLGIOWEPSSRRKPCDCTESWGCIMEETGVSHSRKFSKSTLE 479
 Db 417 GLPMAVAOVLSSLOANLGIOWEPSSRRKPCDCTESWGCIMEETGVSHSRKFSKSTLE 476
 Qy 480 YEDFLORGGACLFNRPKLFPEPTGCGNGYVAGEECDCGFHVECYGCKKCSLSNGAH 539
 Db 477 YEDFLORGGACLFNRPKLFPEPTGCGNGYVAGEECDCGFHVECYGCKKCSLSNGAH 536
 Qy 540 GSDGCCNNTSCLTPRGYECRDVAINECDITEYCTGDSGQCPRLHJHODGYACQONGRC 599
 Db 537 GSDGCCNNTSCLTPRGYECRDVAINECDITEYCTGDSGQCPRLHJHODGYACQONGRC 596
 Qy 600 YNGEKTNDNOCQYIMGTAKAGSDKFCYEKLTGTEKNGKGDGRMIQCSKHDFVCGF 659

Db 597 YNGEKTNDNOCQYIMGTAKAGSDKFCYEKLTGTEKNGKGDGRMIQCSKHDFVCGF 656
 Qy 660 LCTNLTRAPRIGLOIETIPSEFYHOGRVIDSGARVLDLDDYGVYEDGTGCGFSM 719
 Db 657 LCTNLTRAPRIGLOIETIPSEFYHOGRVIDSGARVLDLDDYGVYEDGTGCGFSM 716
 Qy 720 CLDRKLOIALNMSCPLDSKGVCSGHCNEATCICDPTWAGTDCSIDPVRNLHP 779
 Db 717 CLDRKLOIALNMSCPLDSKGVCSGHCNEATCICDPTWAGTDCSIDPVRNLHP 776
 Qy 780 KDEGPKGSATNLIGSIAGAILVAALVIGGTGKGFKNVKKRRPDPQGP 832
 Db 777 KDEGPKGSATNLIGSIAGAILVAALVIGGTGKGFKNVKKRRPDPQGP 829

RESULT 6

US-09-760-484-315
 : Sequence 315, Application US/09760484
 : GENERAL INFORMATION:
 : APPLICANT: Rosen et al.
 : TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 : FILE REFERENCE: PTA3
 : CURRENT APPLICATION NUMBER: US/09/760,484
 : CURRENT FILING DATE: 2001-01-16
 : Prior application data removed - consult PALM or file wrapper
 : NUMBER OF SEQ ID NOS: 638
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 315
 : LENGTH: 776
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: SITE
 : LOCATION: (731)
 : OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 : US-09-760-484-315

Query Match 91.9%; Score 4186; DB 21; Length 776;
 Best Local Similarity 97.8%; Pred. No. 0;
 Matches 759; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 57 AASSRPRAMGAAPAPPHNNTAEKNLGVLADEDTLQONSSNISYSNAOKEITLPSR 116
 Db 1 AASSRPRAMGAAPAPPHNNTAEKNLGVLADEDTLQONSSNISYSNAOKEITLPSR 60
 Qy 117 LIYVINDSESPYHVLDTKARHQQHNKAVHLAQSFOIAFSGKFTLDLILNGLSSD 176
 Db 61 LIYVINDSESPYHVLDTKARHQQHNKAVHLAQSFOIAFSGKFTLDLILNGLSSD 120
 Qy 177 YVEIHYENGKPOYSKGEHCYHGSINGVDSKVALSTCGLHGFEDDTFYVMIPELTD 236
 Db 121 YVEIHYENGKPOYSKGEHCYHGSINGVDSKVALSTCGLHGFEDDTFYVMIPELTD 180
 Qy 237 VHDKSTGRPHIIQKTLAGOYSKOMNLTWERGDOMPELSELOMLKRRRAVNPSCGIFE 296
 Db 181 VHDKSTGRPHIIQKTLAGOYSKOMNLTWERGDOMPELSELOMLKRRRAVNPSCGIFE 240
 Qy 297 EMKYLELMTVNDHKTYKKHRSHTNNFAKSVNLDVSIYEQLNTRVLAVAETWTEK 356
 Db 241 EMKYLELMTVNDHKTYKKHRSHTNNFAKSVNLDVSIYEQLNTRVLAVAETWTEK 300
 Qy 357 DITDITTNPVOMLHEFSKYRQRIKOHADAIVHLISRTFYKRSLSYTGVCSTRGVNEY 416
 Db 301 DITDITTNPVOMLHEFSKYRQRIKOHADAIVHLISRTFYKRSLSYTGVCSTRGVNEY 360
 Qy 417 NEYGLPMAVAOVLSSLOANLGIOWEPSSRRKPCDCTESWGCIMEETGVSHSRKFSKCS 476
 Db 361 NEYGLPMAVAOVLSSLOANLGIOWEPSSRRKPCDCTESWGCIMEETGVSHSRKFSKCS 420
 Qy 477 ILEYRPFLORGGACLFNRPKLFPEPTGCGNGYVAGEECDCGFHVECYGCKKCSLSN 536
 Db 421 ILEYRPFLORGGACLFNRPKLFPEPTGCGNGYVAGEECDCGFHVECYGCKKCSLSN 480

QY 537 GAHCSGPCNNNTSCLFOPRGYECRDVAVNECDITTEYCTGDSGOCPPNLHKODGYACNONC 596
DB 481 GAHCSGPCNNNTSCLFOPRGYECRDVAVNECDITTEYCTGDSGOCPPNLHKODGYACNONC 540
QY 597 GRCYNGECKTRDNOCYIMGTAKAGSDKFCYKLNTEGTEKNGCKGDKGDRWIOCCKIDHVF 656
DB 541 GRCYNGECKTRDNOCYIMGTAKAGSDKFCYKLNTEGTEKNGCKGDKGDRWIOCCKIDHVF 600
QY 657 GCELLCTNLTRAPRIGOLGGEIIPTSFYHOGRIYIDCSGAHVVLDDDTDVGYVEDGTJCGP 716
DB 601 GCELLCTNLTRAPRIGOLGGEIIPTSFYHOGRIYIDCSGAHVVLDDDTDVGYVEDGTJCGP 660
QY 717 SMMCLDRKCLQIOALNMSSCPLDSKGVCSGHGVCNEATCICDFTWAGTDCSIRDPVRN 776
DB 661 SMMCLDRKCLQIOALNMSSCPLDSKGVCSGHGVCNEATCICDFTWAGTDCSIRDPVRN 720
QY 777 LHPKDEGKPSATNLITIGTAGAILVAIYLGGTGWFKNVKKRRFDPDQGP 832
DB 721 LHPKDEGKPSATNLITIGTAGAILVAIYLGGTGWFKNVKKRRFDPDQGP 775

RESULT 7
US-09-631-534-10
Sequence 10, Application US/09631534
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baidur, Nand
APPLICANT: Delsher, Theresa A.
APPLICANT: Bishop, Paul D.
APPLICANT: Taft, David W.
TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
FILE REFERENCE: 98-29C1
CURRENT APPLICATION NUMBER: US/09/631,534
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/092,371
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/147,410
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 709
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-534-10

Query Match 84.6% Score 3851: DB 20: Length 709:
Best Local Similarity 99.7% Pred. No. 4.7e-301:
Matches 699: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

QY 132 LDTKARHQQHKKAVHLAQAFOIEAFSGKFIIDLILNGLSSDYVEIHYENKGPQYSK 191
DB 9 LDTKARHQQHKKAVHLAQAFOIEAFSGKFIIDLILNGLSSDYVEIHYENKGPQYSK 68
QY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGFEDDTFVYMIPELVLVHDEKSTGRPHIIOK 251
DB 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGFEDDTFVYMIPELVLVHDEKSTGRPHIIOK 128
QY 252 TLAGOYSKOMKNTLMERGDOMPFLSELQWLKRRRAVNSRGIFEEMKYLELMIVNDHKT 311
DB 129 TLAGOYSKOMKNTLMERGDOMPFLSELQWLKRRRAVNSRGIFEEMKYLELMIVNDHKT 188
QY 312 YKHHSSHAHTNPNFAKSVNVLVDSTYKEDLNTRVVLVAETWTEKDOIITTPVQMLAE 371
DB 189 YKHHSSHAHTNPNFAKSVNVLVDSTYKEDLNTRVVLVAETWTEKDOIITTPVQMLAE 248
QY 372 FSKYRIRIOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVNVNXYGLPMVAVOYLSQ 431
DB 249 FSKYRIRIOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVNVNXYGLPMVAVOYLSQ 308

QY 432 SLAONLGIOWEPSSRRKPCDCITESMGCCIMETGVSHSRKFSKCSILEYRDLORGCGAC 491
DB 309 SLAONLGIOWEPSSRRKPCDCITESMGCCIMETGVSHSRKFSKCSILEYRDLORGCGAC 368
QY 492 LFNRPYKLFEPTECGNGYVEGECDCGFHYECYGLCKKCSLSGAMCSBGPCCNNTSC 551
DB 369 LFNRPYKLFEPTECGNGYVEGECDCGFHYECYGLCKKCSLSGAMCSBGPCCNNTSC 428
QY 552 LFOPRGYECRDVAVNECDITTEYCTGDSGOCPPNLHKODGYACNONGRCYNECKTRDNOC 611
DB 429 LFOPRGYECRDVAVNECDITTEYCTGDSGOCPPNLHKODGYACNONGRCYNECKTRDNOC 488
QY 612 OYIMGTAKAGSDKFCYKLNTEGTEKNGCKGDKGDRWIOCCKIDHVF 671
DB 489 OYIMGTAKAGSDKFCYKLNTEGTEKNGCKGDKGDRWIOCCKIDHVF 548
QY 672 GOLGGEIIPTSFYHOGRIYIDCSGAHVVLDDDTDVGYVEDGTJCGP 731
DB 549 GOLGGEIIPTSFYHOGRIYIDCSGAHVVLDDDTDVGYVEDGTJCGP 608
QY 732 NMSSCPLDSKGVCSGHGVCNEATCICDFTWAGTDCSIRDPVRNLHPKDEGKPSAT 791
DB 609 NMSSCPLDSKGVCSGHGVCNEATCICDFTWAGTDCSIRDPVRNLHPKDEGKPSAT 668
QY 792 NLIIGTAGAILVAIYLGGTGWFKNVKKRRFDPDQGP 832
DB 669 NLIIGTAGAILVAIYLGGTGWFKNVKKRRFDPDQGP 709

RESULT 8
US-10-260-506-10
Sequence 10, Application US/10260506
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baidur, Nand
APPLICANT: Delsher, Theresa A.
APPLICANT: Bishop, Paul D.
APPLICANT: Taft, David W.
TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
FILE REFERENCE: 98-29C1
CURRENT APPLICATION NUMBER: US/10/260,506
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: 60/092,371
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/147,410
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 709
TYPE: PRT
ORGANISM: Homo sapiens
US-10-260-506-10

Query Match 84.6% Score 3851: DB 26: Length 709:
Best Local Similarity 99.7% Pred. No. 4.7e-301:
Matches 699: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

QY 132 LDTKARHQQHKKAVHLAQAFOIEAFSGKFIIDLILNGLSSDYVEIHYENKGPQYSK 191
DB 9 LDTKARHQQHKKAVHLAQAFOIEAFSGKFIIDLILNGLSSDYVEIHYENKGPQYSK 68
QY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGFEDDTFVYMIPELVLVHDEKSTGRPHIIOK 251
DB 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGFEDDTFVYMIPELVLVHDEKSTGRPHIIOK 128
QY 252 TLAGOYSKOMKNTLMERGDOMPFLSELQWLKRRRAVNSRGIFEEMKYLELMIVNDHKT 311
DB 129 TLAGOYSKOMKNTLMERGDOMPFLSELQWLKRRRAVNSRGIFEEMKYLELMIVNDHKT 188
QY 312 YKHHSSHAHTNPNFAKSVNVLVDSTYKEDLNTRVVLVAETWTEKDOIITTPVQMLAE 371

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Db 189 YKKHRSHTNNFAKSVNLVDSYKEQJNTRVVLAVETWEKDOIITLTPVOYLHE 248
QY 372 FSKYRORIKOHADAVHLISRVTFRHKRSSLSYFGVCSRTRGVAVNEGLPMAVAQVLSQ 431
Db 249 FSKYRORIKOHADAVHLISRVTFRHKRSSLSYFGVCSRTRGVAVNEGLPMAVAQVLSQ 308
QY 432 SLAONLGIOWEPSSRRPKCDCTESWGCIIMEETGVSHSRFSKCSLLEYRDLQRRGGAC 491
Db 309 SLAONLGIOWEPSSRRPKCDCTESWGCIIMEETGVSHSRFSKCSLLEYRDLQRRGGAC 368
QY 492 LFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNTSC 551
Db 369 LFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNTSC 428
QY 552 LFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNTSC 611
Db 429 LFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNTSC 488
QY 612 OYIWTGTRKAAGSDKFCYERKLTETGTEKNGCGKDGDRWIQCSKHDFCGFLCTNLTRAPRI 671
Db 489 OYIWTGTRKAAGSDKFCYERKLTETGTEKNGCGKDGDRWIQCSKHDFCGFLCTNLTRAPRI 548
QY 672 GOLGELIIPSTFYHOGRVIDCSGAHVYLDLDDTVGYVEDTFCGSPSMCLDRKCLQIOL 731
Db 549 GOLGELIIPSTFYHOGRVIDCSGAHVYLDLDDTVGYVEDTFCGSPSMCLDRKCLQIOL 608
QY 732 NMSSCPDLSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKGPAT 791
Db 609 NMSSCPDLSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKGPAT 668
QY 792 NLIISGAILVAIIVLGGTGMFKNKRRRDEPTOOGPI 832
Db 669 NLIISGAILVAIIVLGGTGMFKNKRRRDEPTOOGPI 709

RESULT 9
US-09-631-534-2
; Sequence 2, Application US/09631534
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Tait, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/09/631,534
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147,410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-534-2

Query Match 79.5%; Score 3621; DB 20; Length 696;
Best Local Similarity 99.7%; Pred. No. 1.7e-282;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 132 LDTKARHOKHNAKAVHLAASFOIEAFGSKFTLIDLINLNGLLSSDYVEIHYENKRPQYSK 191
Db 9 LDTKARHOKHNAKAVHLAASFOIEAFGSKFTLIDLINLNGLLSSDYVEIHYENKRPQYSK 68
QY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELVLVHDEKSTGRPHIIOK 251
Db 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELVLVHDEKSTGRPHIIOK 251
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Db 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELVLVHDEKSTGRPHIIOK 128
QY 252 TLAGOSKRMKMLTHERGQMPFSELDLWLRKRRRAVNSRGIFEMEMYLELMTVNDHKT 311
Db 129 TLAGOSKRMKMLTHERGQMPFSELDLWLRKRRRAVNSRGIFEMEMYLELMTVNDHKT 188
QY 312 YKKHRSHTNNFAKSVNLVDSYKEQJNTRVVLAVETWEKDOIITLTPVOYLHE 371
Db 189 YKKHRSHTNNFAKSVNLVDSYKEQJNTRVVLAVETWEKDOIITLTPVOYLHE 248
QY 372 FSKYRORIKOHADAVHLISRVTFRHKRSSLSYFGVCSRTRGVAVNEGLPMAVAQVLSQ 431
Db 249 FSKYRORIKOHADAVHLISRVTFRHKRSSLSYFGVCSRTRGVAVNEGLPMAVAQVLSQ 308
QY 432 SLAONLGIOWEPSSRRPKCDCTESWGCIIMEETGVSHSRFSKCSLLEYRDLQRRGGAC 491
Db 309 SLAONLGIOWEPSSRRPKCDCTESWGCIIMEETGVSHSRFSKCSLLEYRDLQRRGGAC 368
QY 492 LFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNTSC 551
Db 369 LFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNTSC 428
QY 552 LFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNTSC 611
Db 429 LFNRPRTKLEPTECGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNTSC 488
QY 612 OYIWTGTRKAAGSDKFCYERKLTETGTEKNGCGKDGDRWIQCSKHDFCGFLCTNLTRAPRI 671
Db 489 OYIWTGTRKAAGSDKFCYERKLTETGTEKNGCGKDGDRWIQCSKHDFCGFLCTNLTRAPRI 548
QY 672 GOLGELIIPSTFYHOGRVIDCSGAHVYLDLDDTVGYVEDTFCGSPSMCLDRKCLQIOL 731
Db 549 GOLGELIIPSTFYHOGRVIDCSGAHVYLDLDDTVGYVEDTFCGSPSMCLDRKCLQIOL 608
QY 732 NMSSCPDLSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKGPAT 791
Db 609 NMSSCPDLSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKGPAT 664

RESULT 10
US-09-809-617-2
; Sequence 2, Application US/09809617
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-617-2

Query Match 79.5%; Score 3621; DB 22; Length 696;
Best Local Similarity 99.7%; Pred. No. 1.7e-282;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 132 LDTKARHOKHNAKAVHLAASFOIEAFGSKFTLIDLINLNGLLSSDYVEIHYENKRPQYSK 191
Db 9 LDTKARHOKHNAKAVHLAASFOIEAFGSKFTLIDLINLNGLLSSDYVEIHYENKRPQYSK 68
QY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELVLVHDEKSTGRPHIIOK 251
Db 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELVLVHDEKSTGRPHIIOK 128
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OY 252 TLGAOYSKOMKMLTMRGDMPLSELOMLKRRRAVNSRGIPEEMKYLELMIGNDHKT 311
DB 129 TLGAOYSKOMKMLTMRGDMPLSELOMLKRRRAVNSRGIPEEMKYLELMIGNDHKT 188
OY 312 YKRRSSHAHTNNAKSAVNLVDSIYKQOLNTRVLAIVETWEKDOIITTPVOMLHE 371
DB 189 YKRRSSHAHTNNAKSAVNLVDSIYKQOLNTRVLAIVETWEKDOIITTPVOMLHE 248
OY 372 FSKYRORIKOHADAVHLISRVTFFHKKRSSLSYEGVCSRTRGVNEYGLPMAVAOVLQ 431
DB 249 FSKYRORIKOHADAVHLISRVTFFHKKRSSLSYEGVCSRTRGVNEYGLPMAVAOVLQ 308
OY 432 SLAONLGIOMEPSSRKPCKDCTESWGCIIMEETGVSHSRKFSKCSILEYRDFLORGAGAC 491
DB 309 SLAONLGIOMEPSSRKPCKDCTESWGCIIMEETGVSHSRKFSKCSILEYRDFLORGAGAC 368
OY 492 LFNRPRTKLEPTECGNGVYAGEECDGCFHVECYGLCKCKCSLSNGAHCSDBGPCNNITSC 551
DB 369 LFNRPRTKLEPTECGNGVYAGEECDGCFHVECYGLCKCKCSLSNGAHCSDBGPCNNITSC 428
OY 552 LFPGRGYECRDVAINECDITEYCTGDSGQCPPLHLKQDGYACNONOGRCYNGECKTRDNOC 611
DB 429 LFPGRGYECRDVAINECDITEYCTGDSGQCPPLHLKQDGYACNONOGRCYNGECKTRDNOC 488
OY 612 OYIMGTRKAAGSDKFCYEKLTBETGKNGCKDGRMIQCSKHDFVFCGLLCTNLTRA PRI 671
DB 489 OYIMGTRKAAGSDKFCYEKLTBETGKNGCKDGRMIQCSKHDFVFCGLLCTNLTRA PRI 548
OY 672 GOLGELIPTSFYHOGRVIDCSGAHVLLDDPTDVGVEDEGTPCGSPMMLDRKCLQIOAL 731
DB 549 GOLGELIPTSFYHOGRVIDCSGAHVLLDDPTDVGVEDEGTPCGSPMMLDRKCLQIOAL 608
OY 732 NMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKG 787
DB 609 NMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKG 564
```

```
RESULT 11
US-09-809-790-2
; Sequence 2, Application US/09809790
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-790-2
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Query Match 79.5%; Score 3621; DB 22; Length 696;
Best Local Similarity 99.7%; Pred. No. 1.7e-282;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 132 LDTKARHOQKHNKAVHLAQAQSFQIEAFGSKFILDLLINNGLLSSDYVEIHENKGPQYSK 191
DB 9 LDTKARHOQKHNKAVHLAQAQSFQIEAFGSKFILDLLINNGLLSSDYVEIHENKGPQYSK 68
OY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDEKSTGRPHITOK 251
DB 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDEKSTGRPHITOK 128
OY 252 TLGAOYSKOMKMLTMRGDMPLSELOMLKRRRAVNSRGIPEEMKYLELMIGNDHKT 311
DB 129 TLGAOYSKOMKMLTMRGDMPLSELOMLKRRRAVNSRGIPEEMKYLELMIGNDHKT 188
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DB 129 TLGAOYSKOMKMLTMRGDMPLSELOMLKRRRAVNSRGIPEEMKYLELMIGNDHKT 188
OY 312 YKRRSSHAHTNNAKSAVNLVDSIYKQOLNTRVLAIVETWEKDOIITTPVOMLHE 371
DB 189 YKRRSSHAHTNNAKSAVNLVDSIYKQOLNTRVLAIVETWEKDOIITTPVOMLHE 248
OY 372 FSKYRORIKOHADAVHLISRVTFFHKKRSSLSYEGVCSRTRGVNEYGLPMAVAOVLQ 431
DB 249 FSKYRORIKOHADAVHLISRVTFFHKKRSSLSYEGVCSRTRGVNEYGLPMAVAOVLQ 308
OY 432 SLAONLGIOMEPSSRKPCKDCTESWGCIIMEETGVSHSRKFSKCSILEYRDFLORGAGAC 491
DB 309 SLAONLGIOMEPSSRKPCKDCTESWGCIIMEETGVSHSRKFSKCSILEYRDFLORGAGAC 368
OY 492 LFNRPRTKLEPTECGNGVYAGEECDGCFHVECYGLCKCKCSLSNGAHCSDBGPCNNITSC 551
DB 369 LFNRPRTKLEPTECGNGVYAGEECDGCFHVECYGLCKCKCSLSNGAHCSDBGPCNNITSC 428
OY 552 LFPGRGYECRDVAINECDITEYCTGDSGQCPPLHLKQDGYACNONOGRCYNGECKTRDNOC 611
DB 429 LFPGRGYECRDVAINECDITEYCTGDSGQCPPLHLKQDGYACNONOGRCYNGECKTRDNOC 488
OY 612 OYIMGTRKAAGSDKFCYEKLTBETGKNGCKDGRMIQCSKHDFVFCGLLCTNLTRA PRI 671
DB 489 OYIMGTRKAAGSDKFCYEKLTBETGKNGCKDGRMIQCSKHDFVFCGLLCTNLTRA PRI 548
OY 672 GOLGELIPTSFYHOGRVIDCSGAHVLLDDPTDVGVEDEGTPCGSPMMLDRKCLQIOAL 731
DB 549 GOLGELIPTSFYHOGRVIDCSGAHVLLDDPTDVGVEDEGTPCGSPMMLDRKCLQIOAL 608
OY 732 NMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKG 787
DB 609 NMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKG 564
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RESULT 12
US-10-260-506-2
; Sequence 2, Application US/10260506
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/10/260, 506
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-506-2
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Query Match 79.5%; Score 3621; DB 26; Length 696;
Best Local Similarity 99.7%; Pred. No. 1.7e-282;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 132 LDTKARHOQKHNKAVHLAQAQSFQIEAFGSKFILDLLINNGLLSSDYVEIHENKGPQYSK 191
DB 9 LDTKARHOQKHNKAVHLAQAQSFQIEAFGSKFILDLLINNGLLSSDYVEIHENKGPQYSK 68
OY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDEKSTGRPHITOK 251
DB 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDEKSTGRPHITOK 128
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QY 252 TLAQYSKOMKMLTMRGDMPFLSELQWLKRRRAVNPSRGIFEEBKYLELMIVNDHKT 311
 |||||
 Db 129 TLAQYSKOMKMLTMRGDMPFLSELQWLKRRRAVNPSRGIFEEBKYLELMIVNDHKT 188
 |||||
 QY 312 YKHHSSHAHTNNPAKSVNLVDSTYKEQLNTRVLAVETWTEKDQIDITTPVOMLHE 371
 |||||
 Db 189 YKHHSSHAHTNNPAKSVNLVDSTYKEQLNTRVLAVETWTEKDQIDITTPVOMLHE 248
 |||||
 QY 372 FSKYRORIKOHADAVHLISRVTFHYKRSLSYFEGVCSRTRGVNEGYGLPMAVAQVLSQ 431
 |||||
 Db 249 FSKYRORIKOHADAVHLISRVTFHYKRSLSYFEGVCSRTRGVNEGYGLPMAVAQVLSQ 308
 |||||
 QY 432 SLAONLGIOMEPSSRRPKDCCTESMGGCIMEETGVSHSRKFSKCSILEYRDLORGGAC 491
 |||||
 Db 309 SLAONLGIOMEPSSRRPKDCCTESMGGCIMEETGVSHSRKFSKCSILEYRDLORGGAC 368
 |||||
 QY 492 LFNRPTKLEPTECGNGVYEAEBECDGPFHVECYGLCKKCSLSNGAHCSDBGPCNNTSC 551
 |||||
 Db 369 LFNRPTKLEPTECGNGVYEAEBECDGPFHVECYGLCKKCSLSNGAHCSDBGPCNNTSC 428
 |||||
 QY 552 LFOPRGYECRDVNECDITEYCTGDSGQCPNHLKODGYACNONOGRCTNGECKTRDNC 611
 |||||
 Db 429 LFOPRGYECRDVNECDITEYCTGDSGQCPNHLKODGYACNONOGRCTNGECKTRDNC 488
 |||||
 QY 612 QYIMGTAKAGSDKFCYEKLNTEGTEKNGCKDGRWIOCSKHDVFCGFLCTNLTRAPRI 671
 |||||
 Db 489 QYIMGTAKAGSDKFCYEKLNTEGTEKNGCKDGRWIOCSKHDVFCGFLCTNLTRAPRI 548
 |||||
 QY 672 GOLQGEIIPTSFYHOGRVIDCSGAHVYLDLDDTDVGYVEDGTPCGPSMMCLDRKCLQIAL 731
 |||||
 Db 549 GOLQGEIIPTSFYHOGRVIDCSGAHVYLDLDDTDVGYVEDGTPCGPSMMCLDRKCLQIAL 608
 |||||
 QY 732 NMSSCPJDSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRLHPPKDEBPKG 787
 |||||
 Db 609 NMSSCPJDSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRLHPPKDEBPKG 664
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Search completed: June 1, 2003, 18:48:56
 Job time : 826 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2003, 18:17:26 ; Search time 197 Seconds
(without alignments)
874.976 Million cell updates/sec

Title: US-09-634-252A-4
Perfect score: 4553
Sequence: 1 MKPGSSSRPPLAGCSLAG.....GMGFKNKRRPDPTQGPPI 832

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 996614 seqs, 207175905 residues

Total number of hits satisfying chosen parameters: 996614

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA New.*
1: /cgn2-6/ptodata/1/paa/PCU_NEW_COMB.pep.*
2: /cgn2-6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2-6/ptodata/1/paa/US07_NEW_COMB.pep.*
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5: /cgn2-6/ptodata/1/paa/US09_NEW_COMB.pep.*
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7: /cgn2-6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	4553	100.0	832	US-10-359-464-3	Sequence 3, Appl
2	4553	100.0	832	US-10-126-052A-150	Sequence 150, Appl
3	4553	100.0	832	US-10-126-052A-325	Sequence 325, Appl
4	3669	80.6	886	US-09-949-016-11203	Sequence 11203, A
5	1985.5	43.6	870	US-09-724-676-80847	Sequence 80847, A
6	1985.5	43.6	870	US-09-724-676A-80847	Sequence 80847, A
7	1983.5	43.6	899	PCT-US03-04508-64	Sequence 64, Appl
8	1983	43.6	775	US-60-453-135-13204	Sequence 13204, A
9	1983	43.6	775	US-60-453-050-13204	Sequence 13204, A
10	1976.5	43.4	772	US-09-949-016-7315	Sequence 7315, Ap
11	1976.5	43.4	772	US-09-949-016-7315	Sequence 7315, Ap
12	1976.5	43.4	772	US-09-949-016-7315	Sequence 7315, Ap
13	1976.5	43.4	772	US-09-949-016-7315	Sequence 7315, Ap
14	1967	43.2	769	US-09-949-016-9605	Sequence 9605, Ap
15	1967	43.2	769	US-09-949-016-9605	Sequence 9605, Ap
16	1967	43.2	769	US-60-453-135-13202	Sequence 13202, A
17	1967	43.2	769	US-60-453-050-13202	Sequence 13202, A
18	1412.5	31.0	623	US-60-453-050-13203	Sequence 13203, A
19	1412.5	31.0	623	US-60-453-050-13203	Sequence 13203, A
20	1217	26.7	561	US-09-724-676-80848	Sequence 80848, A
21	1217	26.7	561	US-09-724-676-80848	Sequence 80848, A
22	1007.5	22.1	918	US-10-274-639-18	Sequence 18, Appl
23	1007.5	22.1	918	US-10-333-574-18	Sequence 18, Appl
24	1007.5	22.1	918	US-10-405-027-3117	Sequence 3117, Ap
25	986.5	21.7	886	US-60-455-444-4404	Sequence 4404, Ap
26	986.5	21.7	886	US-60-455-241-4404	Sequence 4404, Ap

27	986.5	21.7	923	7	US-60-455-444-4403	Sequence 4403, Ap
28	986.5	21.7	923	7	US-60-465-241-4403	Sequence 4403, Ap
29	986.5	21.7	923	7	US-09-949-016-8262	Sequence 8262, Ap
30	986.5	21.7	968	5	US-09-949-016-11229	Sequence 11229, A
31	967	21.2	914	6	US-10-028-248A-83	Sequence 83, Appl
32	967	21.2	914	6	US-10-107-782-83	Sequence 83, Appl
33	966	21.2	909	1	PCT-US02-19297-78	Sequence 78, Appl
34	966	21.2	909	1	PCT-US02-19592-80	Sequence 80, Appl
35	966	21.2	909	6	US-10-126-052A-427	Sequence 427, App
36	964	21.2	909	6	PCT-US02-37431-2	Sequence 2, Appl
37	964	21.2	909	5	US-09-949-016-6370	Sequence 6370, Ap
38	964	21.2	909	6	US-10-301-822-2	Sequence 2, Appl
39	962.5	21.1	735	6	US-10-145-087A-74	Sequence 74, Appl
40	962.5	21.1	735	6	US-10-145-031A-74	Sequence 74, Appl
41	962.5	21.1	735	6	US-10-145-092A-74	Sequence 74, Appl
42	962.5	21.1	735	6	US-10-162-522A-74	Sequence 74, Appl
43	962.5	21.1	735	6	US-10-165-038A-74	Sequence 74, Appl
44	962.5	21.1	735	6	US-10-165-353-74	Sequence 74, Appl
45	962.5	21.1	735	6	US-10-170-481A-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1
US-10-359-464-3
Sequence 3, Application US/10359464
GENERAL INFORMATION:
APPLICANT: Lopez-Olin, Carlos
APPLICANT: Miguel, Santiago Cal
APPLICANT: Freije, Jose Maria Perez
APPLICANT: Garcia, Jose Manuel Lopez
APPLICANT: Bianchi, Albert Bernard
APPLICANT: Trall, Pamela
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING INTEGRIN-MEDIATED
FILE REFERENCE: D0015 DIV
CURRENT APPLICATION NUMBER: US/10/359,464
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: 09/824,129
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/194,164
PRIOR FILING DATE: 2000-04-03
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
US-10-359-464-3
Query Match 100.0% Score 4553 DB 6 Length 832
Best Local Similarity 100.0% Pred. No. 0
Matches 832: Conservative 0 Mismatches 0 Indels 0 Gaps 0
1 MKPGSSSRPPLAGCSLAGSCGPORGPAGSPAPARTPCRLDLLVLLPLLAAS 60
1 MKPGSSSRPPLAGCSLAGSCGPORGPAGSPAPARTPCRLDLLVLLPLLAAS 60
61 RPRAMGAAPSPAPHNETAENLGLVLADEDTLQONSSNISYSNAMOKEITLPSRLIY 120
61 RPRAMGAAPSPAPHNETAENLGLVLADEDTLQONSSNISYSNAMOKEITLPSRLIY 120
121 INDSSSPYHVLDTKARHOKHMKAVLAQASFOIEAFGSKETLTLNNGLLSSDVEI 180
121 INDSSSPYHVLDTKARHOKHMKAVLAQASFOIEAFGSKETLTLNNGLLSSDVEI 180
181 HYENGRPOYSKGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMEPELVHDE 240
181 HYENGRPOYSKGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMEPELVHDE 240
241 KSTGRPHITOKTLAGYSKMKNLTMERGQWPLSLSLWLKRRKRVNPSRGIFEEKY 300
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Db 241 KSTGRPHIIOKTLAAGYSKOMKNTLWERGDMFPLSEIOMLKRRAVAVNSGJFEEMKY 300
Qy 301 LELMIVNDHKYTKKRRSSHAHTNNFAKSVNLVDSIYKCOLNTRVLAVALVETWTEKDQID 360
Db 301 LELMIVNDHKYTKKRRSSHAHTNNFAKSVNLVDSIYKCOLNTRVLAVALVETWTEKDQID 360
Qy 361 ITTNPVOMLHEFSKYRORIKOHADAHLISRYTFHFKRSSLSYFGVCSRTGAVNEYG 420
Db 361 ITTNPVOMLHEFSKYRORIKOHADAHLISRYTFHFKRSSLSYFGVCSRTGAVNEYG 420
Qy 421 LPMVAQVLSQSLAQNGLIOWEPSSKPKCDCTESMGGCIMEETGVSHSRKFSKCSILEY 480
Db 421 LPMVAQVLSQSLAQNGLIOWEPSSKPKCDCTESMGGCIMEETGVSHSRKFSKCSILEY 480
Qy 481 RDLORGGACLFNRPKLFEPTECGNGVYEAEGECDCGFHVECYGLCKKCSLSNGAHC 540
Db 481 RDLORGGACLFNRPKLFEPTECGNGVYEAEGECDCGFHVECYGLCKKCSLSNGAHC 540
Qy 541 SDGPCNNNTSCLFOPRGYECRDVNECDITEYCTGDSGQCPNMLHODGYACNONOGRCY 600
Db 541 SDGPCNNNTSCLFOPRGYECRDVNECDITEYCTGDSGQCPNMLHODGYACNONOGRCY 600
Qy 601 NGECRTDNOOCYIWTGKAAGSDKFCYEKLTETEGKNGCKDGRWIOCSKHDFCGFL 660
Db 601 NGECRTDNOOCYIWTGKAAGSDKFCYEKLTETEGKNGCKDGRWIOCSKHDFCGFL 660
Qy 661 LCTNLTTRAPRIGOLGEIIPTSFYHOGRVIDCSGAHVLDLDDTVGYVEDGTGCGPSMMC 720
Db 661 LCTNLTTRAPRIGOLGEIIPTSFYHOGRVIDCSGAHVLDLDDTVGYVEDGTGCGPSMMC 720
Qy 721 LDRKCLIOALNMSSCPDLSKGVCSGHGVSNEATCICDTWAGTDCSIRDVPRNLHP 780
Db 721 LDRKCLIOALNMSSCPDLSKGVCSGHGVSNEATCICDTWAGTDCSIRDVPRNLHP 780
Qy 781 KDEGPKGPSATNLLIGSISAGAILVAAILVGGTGMGFKVKKRRRDPDPOQGP 832
Db 781 KDEGPKGPSATNLLIGSISAGAILVAAILVGGTGMGFKVKKRRRDPDPOQGP 832

RESULT 2
US-10-126-052A-150
: Sequence 150, Application US/10126052A
: GENERAL INFORMATION:
: APPLICANT: Murray, Richard
: APPLICANT: Aziz, Natasha
: TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
: FILE REFERENCE: 018501-001530US
: CURRENT APPLICATION NUMBER: US/10/126,052A
: CURRENT FILING DATE: 2002-04-18
: PRIOR APPLICATION NUMBER: US 60/284,770
: PRIOR FILING DATE: 2001-04-18
: PRIOR APPLICATION NUMBER: US 60/290,492
: PRIOR FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: US 60/339,245
: PRIOR FILING DATE: 2001-11-09
: PRIOR APPLICATION NUMBER: US 60/350,666
: PRIOR FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US 60/334,370
: PRIOR FILING DATE: 2001-11-29
: PRIOR APPLICATION NUMBER: US 60/372,246
: PRIOR FILING DATE: 2002-04-12
: NUMBER OF SEQ ID NOS: 691
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 150
: LENGTH: 832
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-126-052A-150

Query Match 100.0%; Score 4553; DB 6; Length 832;
Best Local Similarity 100.0%; Pred. No. 0;

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Matches 832: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKPGSSSRPPPLACCSISAGSCGPORGPASVASAPRPPCRLLVLLLPPLAAS 60
Db 1 MKPGSSSRPPPLACCSISAGSCGPORGPASVASAPRPPCRLLVLLLPPLAAS 60
Qy 61 RPRWGAAPSPAHNNTAEKMLGVLADEDNLTQONSSNISYSNAMKEITLPSRLIY 120
Db 61 RPRWGAAPSPAHNNTAEKMLGVLADEDNLTQONSSNISYSNAMKEITLPSRLIY 120
Qy 121 INODESPYHVLDTKARHQQKHNKAHVLAQSFQIEAGSKFIIDLINNGLSSDYEI 180
Db 121 INODESPYHVLDTKARHQQKHNKAHVLAQSFQIEAGSKFIIDLINNGLSSDYEI 180
Qy 181 HYENKRPQYKSGEHCYHYGSIIRGYKDSVALSTCNGLHGMEDDTFYMIETPLEVDE 240
Db 181 HYENKRPQYKSGEHCYHYGSIIRGYKDSVALSTCNGLHGMEDDTFYMIETPLEVDE 240
Qy 241 KSTGRPHIIOKTLAAGYSKOMKNTLWERGDMFPLSEIOMLKRRAVAVNSGJFEEMKY 300
Db 241 KSTGRPHIIOKTLAAGYSKOMKNTLWERGDMFPLSEIOMLKRRAVAVNSGJFEEMKY 300
Qy 301 LELMIVNDHKYTKKRRSSHAHTNNFAKSVNLVDSIYKCOLNTRVLAVALVETWTEKDQID 360
Db 301 LELMIVNDHKYTKKRRSSHAHTNNFAKSVNLVDSIYKCOLNTRVLAVALVETWTEKDQID 360
Qy 361 ITTNPVOMLHEFSKYRORIKOHADAHLISRYTFHFKRSSLSYFGVCSRTGAVNEYG 420
Db 361 ITTNPVOMLHEFSKYRORIKOHADAHLISRYTFHFKRSSLSYFGVCSRTGAVNEYG 420
Qy 421 LPMVAQVLSQSLAQNGLIOWEPSSKPKCDCTESMGGCIMEETGVSHSRKFSKCSILEY 480
Db 421 LPMVAQVLSQSLAQNGLIOWEPSSKPKCDCTESMGGCIMEETGVSHSRKFSKCSILEY 480
Qy 481 RDLORGGACLFNRPKLFEPTECGNGVYEAEGECDCGFHVECYGLCKKCSLSNGAHC 540
Db 481 RDLORGGACLFNRPKLFEPTECGNGVYEAEGECDCGFHVECYGLCKKCSLSNGAHC 540
Qy 541 SDGPCNNNTSCLFOPRGYECRDVNECDITEYCTGDSGQCPNMLHODGYACNONOGRCY 600
Db 541 SDGPCNNNTSCLFOPRGYECRDVNECDITEYCTGDSGQCPNMLHODGYACNONOGRCY 600
Qy 601 NGECRTDNOOCYIWTGKAAGSDKFCYEKLTETEGKNGCKDGRWIOCSKHDFCGFL 660
Db 601 NGECRTDNOOCYIWTGKAAGSDKFCYEKLTETEGKNGCKDGRWIOCSKHDFCGFL 660
Qy 661 LCTNLTTRAPRIGOLGEIIPTSFYHOGRVIDCSGAHVLDLDDTVGYVEDGTGCGPSMMC 720
Db 661 LCTNLTTRAPRIGOLGEIIPTSFYHOGRVIDCSGAHVLDLDDTVGYVEDGTGCGPSMMC 720
Qy 721 LDRKCLIOALNMSSCPDLSKGVCSGHGVSNEATCICDTWAGTDCSIRDVPRNLHP 780
Db 721 LDRKCLIOALNMSSCPDLSKGVCSGHGVSNEATCICDTWAGTDCSIRDVPRNLHP 780
Qy 781 KDEGPKGPSATNLLIGSISAGAILVAAILVGGTGMGFKVKKRRRDPDPOQGP 832
Db 781 KDEGPKGPSATNLLIGSISAGAILVAAILVGGTGMGFKVKKRRRDPDPOQGP 832

RESULT 3
US-10-126-052A-325
: Sequence 325, Application US/10126052A
: GENERAL INFORMATION:
: APPLICANT: Murray, Richard
: APPLICANT: Aziz, Natasha
: TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
: FILE REFERENCE: 018501-001530US
: CURRENT APPLICATION NUMBER: US/10/126,052A
: CURRENT FILING DATE: 2002-04-18
: PRIOR APPLICATION NUMBER: US 60/284,770
: PRIOR FILING DATE: 2001-04-18

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PRIOR APPLICATION NUMBER: US 60/290,492
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 60/339,245
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/334,370
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 691
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 325
LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
US-10-126-052A-325

Query Match 100.0%; Score 4553; DB 6; Length 832;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKPPGSSSRPPPLAGCSLAGASCGPQGRPAGSVAPAPARTPPCRLVLLPLPLASS 60
QY 61 RPRAMGAAPAPAPMNETAEKNLGLADEDNLTLOONSSNITSYANMOKETLPSPRLTY 120
DB 61 RPRAMGAAPAPAPMNETAEKNLGLADEDNLTLOONSSNITSYANMOKETLPSPRLTY 120
QY 121 INODESPYHVLDTKARHQRKNRAVHLAQSFOLEAGSKFIIDLINGLSSDYVEI 180
DB 121 INODESPYHVLDTKARHQRKNRAVHLAQSFOLEAGSKFIIDLINGLSSDYVEI 180
QY 181 HYEKGKPOYSKGGHCYHNGSIRGVKDSKVALSTCNGHGMEDDTFYMIPELVLNDE 240
DB 181 HYEKGKPOYSKGGHCYHNGSIRGVKDSKVALSTCNGHGMEDDTFYMIPELVLNDE 240
QY 241 KSTGRPHIIOKTLAGQYSKQKMLTMRGDMFELSLOLMLKRRRAVPSRGIFEEMKY 300
DB 241 KSTGRPHIIOKTLAGQYSKQKMLTMRGDMFELSLOLMLKRRRAVPSRGIFEEMKY 300
QY 301 LELMIVNDHKTYYKRRSSHAHTNPFKSVNLVDSIYEQLNTRVYLVAETWTERDOID 360
DB 301 LELMIVNDHKTYYKRRSSHAHTNPFKSVNLVDSIYEQLNTRVYLVAETWTERDOID 360
QY 361 ITTPVOMLHEFSKYRORIKQHADAVHLISRVTFFYKRRSSLSYFGVCSRTGAVNEGY 420
DB 361 ITTPVOMLHEFSKYRORIKQHADAVHLISRVTFFYKRRSSLSYFGVCSRTGAVNEGY 420
QY 421 LPMVAQVLSOSLAQNLGQIOWEPSSRRPKDCCTESMGCCIMEETGVSHSRKSKSILEY 480
DB 421 LPMVAQVLSOSLAQNLGQIOWEPSSRRPKDCCTESMGCCIMEETGVSHSRKSKSILEY 480
QY 481 RDLQORGAGACLFNRPTKLFEPTECGNGYVEAGEECDCGFHVECYGLCKKCSLSHAGC 540
DB 481 RDLQORGAGACLFNRPTKLFEPTECGNGYVEAGEECDCGFHVECYGLCKKCSLSHAGC 540
QY 541 SDGFCNNNTSCLFPRGVEGRDAVNECDITEYCTGDSQCCPNLHKOGYACNONMGXY 600
DB 541 SDGFCNNNTSCLFPRGVEGRDAVNECDITEYCTGDSQCCPNLHKOGYACNONMGXY 600
QY 601 NGECKTRDNOCQYIMGTKAAGSDKFCYEKLNTETGEKNGCKGDKGRWIOCSKHADVCGTL 660
DB 601 NGECKTRDNOCQYIMGTKAAGSDKFCYEKLNTETGEKNGCKGDKGRWIOCSKHADVCGTL 660
QY 661 LCTNLTRAPRIGOLGELIPTSFYHOGGRVIDCSGAHVVLDDDTDVGYVEDGTPCGPSMVC 720
DB 661 LCTNLTRAPRIGOLGELIPTSFYHOGGRVIDCSGAHVVLDDDTDVGYVEDGTPCGPSMVC 720
QY 721 LDRKCLQIOALNMSSCPIDSKGKVCSGHGVCSNEATCICDFTWAGTDCSIRPVRNLHP 780
DB 721 LDRKCLQIOALNMSSCPIDSKGKVCSGHGVCSNEATCICDFTWAGTDCSIRPVRNLHP 780

QY 781 KDEGPKPSATNLIIISAGAILVAIVLGTGCGFKNNKRRRDEPTQCGPI 832
DB 781 KDEGPKPSATNLIIISAGAILVAIVLGTGCGFKNNKRRRDEPTQCGPI 832

RESULT 4
US-09-949-016-11203

Sequence 11203, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11203

LENGTH: 686

TYPE: PRT

ORGANISM: Human

US-09-949-016-11203

Query Match 80.6%; Score 3669; DB 5; Length 686;
Best Local Similarity 100.0%; Pred. No. 1,2e-277;

Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GLSSSYVEIHENGRPOYSKGGHCYHNGSITGVYDSKVALSTCNGHGMEDDTFYVM 230
DB 25 GLSSSYVEIHENGRPOYSKGGHCYHNGSITGVYDSKVALSTCNGHGMEDDTFYVM 84
QY 231 IPELTVHDEKSTGRPHIIOKTLAGQYSKQKMLTMRGDMFELSLOLMLKRRRAVNP 290
DB 85 IPELTVHDEKSTGRPHIIOKTLAGQYSKQKMLTMRGDMFELSLOLMLKRRRAVNP 144
QY 291 SNGIFEEMKYLELMIVNDHKTYYKRRSSHAHTNPFKSVNLVDSIYEQLNTRVYLVAV 350
DB 145 SNGIFEEMKYLELMIVNDHKTYYKRRSSHAHTNPFKSVNLVDSIYEQLNTRVYLVAV 204
QY 351 EMTWTERDOIDITTPVOMLHEFSKYRORIKQHADAVHLISRVTFFYKRRSSLSYFGVCSR 410
DB 205 EMTWTERDOIDITTPVOMLHEFSKYRORIKQHADAVHLISRVTFFYKRRSSLSYFGVCSR 264
QY 411 TFGVGVNEGLPMAVAVQVLSOSLAQNLGQIOWEPSSRRPKDCCTESMGCCIMEETGVSHSR 470
DB 265 TFGVGVNEGLPMAVAVQVLSOSLAQNLGQIOWEPSSRRPKDCCTESMGCCIMEETGVSHSR 324
QY 471 KFSKCSILEYRDLQORGAGACLFNRPTKLFEPTECGNGYVEAGEECDCGFHVECYGLCK 530
DB 325 KFSKCSILEYRDLQORGAGACLFNRPTKLFEPTECGNGYVEAGEECDCGFHVECYGLCK 384
QY 531 KCSLSHAGCSDGPPCCNNNTSCLFPRGVEGRDAVNECDITEYCTGDSQCCPNLHKOGY 590
DB 385 KCSLSHAGCSDGPPCCNNNTSCLFPRGVEGRDAVNECDITEYCTGDSQCCPNLHKOGY 444
QY 591 ACNONGRCYNGECKTRDNOCQYIMGTKAAGSDKFCYEKLNTETGEKNGCKGDKGRWIOCSKHADVCGTL 650
DB 445 ACNONGRCYNGECKTRDNOCQYIMGTKAAGSDKFCYEKLNTETGEKNGCKGDKGRWIOCSKHADVCGTL 504
QY 651 SKHDVFCGELCTNLTRAPRIGOLGELIPTSFYHOGGRVIDCSGAHVVLDDDTDVGYVED 710
DB 505 SKHDVFCGELCTNLTRAPRIGOLGELIPTSFYHOGGRVIDCSGAHVVLDDDTDVGYVED 564
QY 711 GTPCGPSMVCIDRKCLQIOALNMSSCPIDSKGKVCSGHGVCSNEATCICDFTWAGTDCSIRPVRNLHP 770
DB 565 GTPCGPSMVCIDRKCLQIOALNMSSCPIDSKGKVCSGHGVCSNEATCICDFTWAGTDCSIRPVRNLHP 624


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Db 498 PMGTVCREAVNDCDIRETCGNSQCAPNHHKMDGSCDVGOCICFGRCRCKTRDROCKYI 557
Oy 615 WGTKAAGSKFCYEKLTGTEKNGCKGKDDRWIOCSKHDFVCGFLLCTNLTRAIRIGOL 674
Db 558 WQKVATASDKYCEKLTGTEKNGCKGKDDRWIOCSKHDFVCGFLLCTNLTRAIRIGOL 617
Oy 675 QGEIIPTSFYHOGRVIDCSGAHVLLDDDTDVGVVEGCTPCGSPMCLDRKCLQIOALNMS 734
Db 618 DGEITSTLVVQGGRTLNCSGGHVKKLEEDVDLGVVEDGTCGCPQMKLEHRCPLVASFNFS 677
Oy 735 SCPLDSKGVCSGHGVCNEATCICDFTWAGTDCSIRDPVNLHPKDEGPK----- 786
Db 678 TGLSKRGTCISGNGVCNMLKVCNRMHIGSDC-----NTYFPINDAKTGITLSGN 730
Oy 787 GPSATNLIIGSAGAILVAIVLGGTGKGFKNVKKRR 823
Db 731 GVAGTNIIGIAGTILVLAIVLIGITAMGYKNVREOR 767

```

RESULT 7

```

PCT-US03-04508-64
Sequence 64, Application PC/TUS0304508
GENERAL INFORMATION:
APPLICANT: IDEC PHARMACEUTICALS
APPLICANT: GATELEY, DENNIS
TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF IN DESIGN
FILE REFERENCE: 03/003/0301985
CURRENT APPLICATION NUMBER: PCT/US03/04508
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
LENGTH: 899
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-04508-64

```

```

Query Match 43.6%; Score 1983.5; DB 1: Length 899;
Best Local Similarity 47.5%; Pred. No. 6,4e-146;
Matches 388; Conservative 121; Mismatches 227; Indels 81; Gaps 14;

```

```

Oy 36 SAPARTPCRLILVLLPLLAASSRRPAAAPAPAHMNETAEKNLGVLADEDNLTLOO 35
Db 3 AAVAVSVPLLLCVLTCTCPARC-----GQAGDASLMELEKREN----- 42
Oy 96 NSSSNISYSANAMOKETLPSRLIYINODESPYHVLDTKARHQQHKAHLAQAQSFJ1 155
Db 43 -----RFEQROGIVPLRLIYRSGGEDESHHDLDTFRGDLGQPLTHVDAQSFVY 93
Oy 156 EAFGSKFILDILNNLLSSDYVEIHYEN-GKPOYSKGEHCYHGSIRKVKSKVALST 214
Db 94 DAFGTSFILDVVLNHLSEYIERHIEHGKTVKVEYKGGECYQGIKRNPSFVALST 153
Oy 215 CNGLHGMFEDDTFVYMEIPELVLHDEKSTGRP-----HIQKTLAQYSK-----OMKN 263
Db 154 CNGLHGMFEDDTFVYMEIPELVLHDEKSTGRP-----HIQKTLAQYSK-----OMKN 263
Oy 264 LTMERCDQPPFSELOMLKRRRAVNPSCGIFEDMKYLELMIYNDKRTYKHHSSHAHVN 323
Db 209 ITPSK-----FLIKPPKRSKRLRRYPRNVEETRYIELMIYNDHLMFKHRLSYVHCN 263
Oy 324 NFAKSVVNLVDSYKXOLNTRVLAVENTEKQDIDITNPQOMLHEFSKYROR-1KOH 382
Db 264 TYAKSVVNMADLIYKQDLKTRIVLAMEWTATDNKFAISENPPLITLREFMKRYRDPITKIX 323

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Oy 383 ADAVHLISRVTFHYKRRSLSPFGVCSRTRGVGNEXLEYLPMAAVLAQVLSQSLAQIOWE 442
Db 324 SDAVHLEFSSQSFESSRGAIVIGIGICSLKGGVNERGKIDMAVTLAQSLAHNIGI--- 380
Oy 443 PSSRRKP-----CDCTESMGCIMETGVSHSRKFSKSLLEYRDLQRCGACLEFRPT 497
Db 381 -ISDKRKLASGECEPDYMSGCJIMGDGYVLPKFKTCNIEEYHDFLNSGGACLPFKPS 439
Oy 498 KLEPPECGNGVYAGECCCGFVBCY-----GLCCRKCSLSNAGHCSGDCPCNNTSCLFQ 554
Db 440 KLDPPRCGNGFLETGECDCGTPRAECVLGAECCKCTTLTQDSQSDGJCK--KKFQ 497
Oy 555 PRGVECDVAVNEDITFCTGDSQCPRNLHKODVACNNOGVCYGECKTRPNOCVY 614
Db 498 PMGTVCREAVNDCDIRETCGNSQCAPNHHKMDGSCDVGOCICFGRCRCKTRDROCKYI 557
Oy 615 WGTKAAGSKFCYEKLTGTEKNGCKGKDDRWIOCSKHDFVCGFLLCTNLTRAIRIGOL 674
Db 558 WQKVATASDKYCEKLTGTEKNGCKGKDDRWIOCSKHDFVCGFLLCTNLTRAIRIGOL 617
Oy 675 QGEIIPTSFYHOGRVIDCSGAHVLLDDDTDVGVVEGCTPCGSPMCLDRKCLQIOALNMS 734
Db 618 DGEITSTLVVQGGRTLNCSGGHVKKLEEDVDLGVVEDGTCGCPQMKLEHRCPLVASFNFS 677
Oy 735 SCPLDSKGVCSGHGVCNEATCICDFTWAGTDCSIRDPVNLHPKDEGPK----- 786
Db 678 TGLSKRGTCISGNGVCNMLKVCNRMHIGSDC-----NTYFPINDAKTGITLSGN 730
Oy 787 GPSATNLIIGSAGAILVAIVLGGTGKGFKNVKKRR 823
Db 731 GVAGTNIIGIAGTILVLAIVLIGITAMGYKNVREOR 767

```

RESULT 8

```

US-60-453-135-13204
Sequence 13204, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARCILL, Michele
APPLICANT: TAKUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CLO01456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13204
LENGTH: 775
TYPE: PRT
ORGANISM: Homo sapiens
US-60-453-135-13204

```

```

Query Match 43.6%; Score 1983; DB 7: Length 775;
Best Local Similarity 48.7%; Pred. No. 5.9e-146;
Matches 398; Conservative 92; Mismatches 225; Indels 102; Gaps 17;

```

```

Oy 46 LLLVLLPLLAASSRRPRA--WGA-----AAPSAHPMNETAEKNLGVLADEDNLTLOUNSS 99
Db 12 LLLSLPPTPGIGTGGPAGALRMGGLPOLGCTGAP----- 45
Oy 100 NISYSANAMOKETLPSRLIYINODESPYHVLDTKARHQQHKAHLAQAQSFIEAFG 159
Db 46 -----EVEFSPSLVRE--SSGGEYRKQODLTRVROEPRGGRPHLAQVSVIAPFN 94
Oy 160 SKPLDILNLNGLLSSDYVEIHY-ENKGPQYSK-GEHCYHGSIRGVKDSKVALSTCNG 217
Db 95 SNFPLDLELNNHLLSSQYVERHFSREGTQHSAGCHCYQGRKLRGNPHSFAALSTCOG 154
Oy 218 LHMFEEDDTFVYMEIPELV--HDEKSTGRPHIIOKTLAQYSKOMNLTMERCDQPPFL 275
Db 155 LHGVFSGNLTYIVEPQEVAGPWCAPGCPPLHLIYR-----PLL 194
Oy 276 SELQWLK-----RRKRAVNPSCG--IFEDMKYLELMIYNDHKTXY 312

```


[illegible]

```

? PRIOR APPLICATION NUMBER: 60/723,458
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SFO ID NOS: 207012
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SFO ID NO: 7315
? LENGTH: 772
? TYPE: PRT
? ORGANISM: Human
US-09-949-016-7315

```

Query Match 43.4%; Score 1976.5; DB 5; Length 772;
Best Local Similarity 47.5%; Pred. NO. 1.9e-145;
Matches 388; Conservative 118; Mismatches 229; Indels , 81; Gaps 14;

```

0Y 31 GSVAPASAPRPPCLLVLLVLLLPRLAASSRBRAGAAAPAPHNNEFAEKNLGVLAED 90
Db 9 GSTMOAAVAASVPFLLLCVLGTCGPARC-----GQAGDASLMELEKREN----- 53
0Y 91 NTLQOONSSNLSYSNAMOKEITLPSRLYYINODESESYHVLDTPKARHQOKHNKAVHLAQ 150
Db 54 -----RVEROSITVPLRLLYRSGDESESHDLDTPRVRRDLCGPOLTHDQ 99
0Y 151 ASFOIEAFSGFILLDLINNLGLSSDYVEIHVEN-GKPOYSKGEGHCYHGSIRGVKDSK 209
Db 100 ASFOVDNAGTGFILDDVYNLHDHLLSEYIERHIEHOGKATVEYKGGHCYQOGRINPDSF 159
0Y 210 VALSTCNLHGAFEDDFVYMIERPLELVHDEKSTGRP---HIOKTLAGQYSK----- 259
Db 160 VALSTCHLHGMFYGNHTYLIER-----EENDTQOEOPHFHSYKSRSLFEFSLDDLPSE 214
0Y 260 -OMNKLIMERDDQMFSELQWMLKRRKAAVNSRQIEEMYLEMTYINOHKTYKKHRS 318
Db 215 FOQVNTPSK----FLKPRKRSKROLRRYPRVVEETTYIELMTINDHLMFKHRLS 269
0Y 319 HAHTNNAFSAVYNLVDYSYKEDOLNRRVVLAVAVETTEEODIDITPNPOMLHEFSKYROR 378
Db 270 VVHTNTYKASVYNNMADLITKOLKTRIVLYAMEMTATDNKFAISNPLITLREFKATYRD 329
0Y 379 -IKOHADAVHLISRVTFFHYKSSLSYFGCVCSKRTRGVAVNEYGLPMAVAOVLSSOLAOL 437
Db 330 FIKESDSVAVHLFSGQSFSSRSAGVAYIGITSLKGGGVNBERGKTDLMAVTLAOSLANHI 389
0Y 438 G1OMEPSRRPK-----CDTRESMCGCIIMEEYVSHSRFSKCSITLEYRDLORGGACL 492
Db 390 GI-----ISDKRRLASGECCEDTWMSGCIMGDTGYLLPKKFTQCNIEETHDPLNSGGACL 445
0Y 493 FNRPTKLEPTEPCNGVYEEBECDCGFHVECY---GLJCKKCSLSNGAHCSDGBCNNT 549
Db 446 FNKPSKLLDPBECGNGFIETGEBECDCGRPAEVLGABACCKKCTULTQDSOGSDGLCK-- 503
0Y 550 SCLTOPRGYECRDVANECDITETCYTGDSGQCPPLNKHODGYACNONGRCYNGEKTARDN 609
Db 504 KCFQPMQTYCREAANDCDIRECTCGNSNOCAPNIIHKMDGVSCLDDVOJICFGRCKTDR 563
0Y 610 QCOYIMGKKAASDKFCYEKLENTBETSEKNGCCKDDRMIOCSKHNDFVCGFLLCTUYNTRAP 669
Db 564 OCKYIMGKAVLASDKCYCEKLENTBETSEKNGCKODMYIQCNRKRYLDCGYLLCTIYGINP 623
0Y 670 RIGQLOGEIIPTSFYHOGRVIDCSGAHVLDLDDTDVGVVEDGTPCGPSMCLDRKCLQIQ 729
Db 624 RIGLEDGETITSLVYQOGRITLNSGHHKLELDEVDVLGVVEDGTPCGPMOCLNHRCLPYA 683
0Y 730 ALNMSSCPLDSDGKAYCSHGVCNSNATYICDPTAGTGCSTIRDPVRNLHPRDEBPK--- 786
Db 684 SFNESTCLSSKEGTICSGNGVCNKLKVCVNNHMGSDC-----NTYFPHNDAKKGI 736
0Y 787 -----GSPATNLIIGSIGAILVAIVLAVGTGCMGR 817
Db 737 TLSGNGVACTNIIIGIAGTILVALIIGITAMKIX 772

```

```

; Sequence 7316, Application us/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: fastseq for windows version 4.0
; SEQ ID NO 7316
; LENGTH: 772
; TYPE: PRF
; ORGANISM: Human
US-09-949-016-7316

```

Query Match 43.4%; Score 1976.5; DB 5; Length 772;

Best Local Similarity 47.5%; Pred. No. 1.9e-145;

Matches 388; Conservative 118; Mismatches 229; Indels 81; Gaps 14;

```

OY 31 GVPASAPARTPPCRLLVLLPLPLAASSRRAMGAAPSAPHWNETAEKNLGVLADED 90
DB 9 GSTMAAIVAVSVFELLCVGTCPARC-----GAGDASLMELEKREN----- 53
OY 91 NTLQONSSNISYSNMAKEITLPSRLIYINODESPYHVDTKARHQOKHNKAVHLAQ 150
DB 54 -----RVERQSIPLRLIYRSGGEDESRHDALDTRVGDLGQPLTHVDQ 99
OY 151 ASFOIFAFSGKELDLILNGLISDYVEIHEN-GKPOYSKSGEHYHGSTRGVYDSK 209
DB 100 ASFOVAFGTSFLDVLNHLDLSEYIERHIEHGKTYEVKGEHCYOGHIRGNPDSF 159
OY 210 VALSTNGHGMEDDTEFVMIPELVLHDEKSTGRP---HIIOKTLAOGYSK----- 259
DB 160 VALSTGHGFMFDGNHLYLER-----ENDTTOEDFHFHSYKRLFEFSLDDLPSE 214
OY 260 -QMKNLTMERGDMPLSELQWLKRRRAVNPGRGIFEEKYLEMLVNDHKTYKRRSS 318
DB 215 FQOVNITPSK-----FILKPRPKRSKQLRRYPRNVEEFKTYELMIVNDHMKRHLS 269
OY 319 HATNNFAVSVALVDSIYKEQLNTRVYLAVENTEKQDIDITTNPVOMLHESKYROR 378
DB 270 VVHTNTYASVMMADLTYDQDKTRIVLAVMETWATDNKFAISENPLITLREPMKTRD 329
OY 379 -IKOHADAVHLISRVTFFHRRSSLSYFGVCSRTRGVNEGYLPMVAQVLSQSLAQL 437
DB 330 FIKKSDAVHLFGSGOFESSRSGAAYIGICSLKGGVNEFGKTDLMAVTLAOSLANI 389
OY 438 GIGMESSSRPK-----CDCTESWGCIMETGVSHRSKFSKSLLEYRDFLORGACL 492
DB 390 GI-----ISDKRKLASGCEKCEDTWSGCMIDTYLPRKFTQCNIIEYHDFLNSGGACL 445
OY 493 FNRPTKLFEPTEGNGVVEAGEEDCGFHECY---GLCCKKCSLSNGAHCSDPCCNNT 549
DB 446 FNRPSKLLDPECGNGFETGEBDCGTPAECVLEGAECCKKCTLTODSQCSDGLCK-- 503
OY 550 SCLFOPRGYECRAVNECDITTEYCTGSDGOCPPNLHRODGYACNQNOGRCYNGECKTRDN 609
DB 504 KCKRQPMGTVCRAEVNCDIRETCSGNSQCAPNIIHKMDYSGDVGOCIGFGRCRTRDR 563
OY 610 QCOITMGTAKAGSDKFCYEKINTGTEKNGKGDGDMIOCSKHVDVFCGFLCTNLTRAP 669
DB 564 QCKYIMOKYATASDKYCEKINTEKNGKGDGDMIOCNKRVDYLCGYLLCTNIGNIP 623
OY 670 RIGLOGEIITPTSYHOGRAVLDSCAGAVLDDDTDVGVEEDGTPCGSPMCLDRKCLQIQ 729
DB 624 RLGLDELTSTLVVQGRTLNCSGHVLEEDVLDGIVEDEGTPCGPOMCLERHCLFVA 683

```

```

OY 730 ALNMSSCPDLSKGVCSGHCNSENATCICDFTWAGTDCSIRDPVNNLHPPKDEGPK--- 786
DB 684 SFNFSTCLSKREKSTICSGNVCNSELKVCNRRHWISSDC-----NTYFPHNDAKTGI 736
OY 787 -----GPSATNLLIGSIAGAILVAIVLGGTGMGFK 817
DB 737 TLGNGVAGTNIIIGIAGTILVALILGITAMGYK 772

```

Search completed: June 1, 2003, 18:52:27
Job time: 198 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2003, 16:58:30 : Search time 58 Seconds
(without alignments)
422.067 Million cell updates/sec

Title: US-09-634-252a-4

Perfect score: 4553

Sequence: 1 MKPSSSSKQPLACGSLAG.....GNGFKVKKRRRDPDQGP1 832

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents, AA:*
1: /cgcn2_6/pcodata/1/1aa/5a_COMB.pep:*
2: /cgcn2_6/pcodata/1/1aa/5b_COMB.pep:*
3: /cgcn2_6/pcodata/1/1aa/5a_COMB.pep:*
4: /cgcn2_6/pcodata/1/1aa/5b_COMB.pep:*
5: /cgcn2_6/pcodata/1/1aa/5a_COMB.pep:*
6: /cgcn2_6/pcodata/1/1aa/5b_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3621	79.5	696	4	US-09-351-414-2
2	1978	43.4	769	1	US-08-243-542-4
3	1978	43.4	769	1	US-08-477-407-4
4	1978	43.4	769	1	US-08-484-355-4
5	1867.5	41.0	670	1	US-08-243-542-3
6	1867.5	41.0	670	1	US-08-477-407-3
7	1867.5	41.0	670	1	US-08-484-355-3
8	1297	28.5	524	1	US-08-243-542-2
9	1297	28.5	524	1	US-08-477-407-2
10	1297	28.5	524	1	US-08-484-355-2
11	1293	28.4	488	1	US-08-243-542-1
12	1293	28.4	488	1	US-08-477-407-1
13	1293	28.4	488	1	US-08-484-355-1
14	897	19.7	812	4	US-09-632-098-4
15	897	19.7	812	4	US-09-632-098-2
16	897	19.7	812	4	US-09-632-098-1
17	837	18.4	855	4	US-09-813-819-2
18	837	18.4	855	4	US-09-813-819-1
19	829	18.2	751	2	US-08-836-443-3
20	826	18.1	814	4	US-09-813-819-4
21	772.5	17.0	613	4	US-09-920-048-4
22	766.5	16.8	621	4	US-09-920-048-10
23	751.5	16.5	621	4	US-09-026-001A-18
24	749	16.5	621	4	US-09-026-001A-6
25	739	16.2	734	5	US-09-026-001A-14
26	739	16.2	734	5	US-08-765-243-8
27	736	16.2	616	4	PCT-US95-07295-8

28	711	15.6	651	1	US-08-264-101-2	Sequence 2, Appl1
29	711	15.6	651	2	US-08-765-243-2	Sequence 2, Appl1
30	711	15.6	651	5	PCT-US95-07295-2	Sequence 2, Appl1
31	691	15.2	735	2	US-08-765-243-6	Sequence 6, Appl1
32	691	15.2	735	5	PCT-US95-07295-6	Sequence 6, Appl1
33	649	14.3	521	4	US-09-026-001A-12	Sequence 12, Appl1
34	611	13.4	462	4	US-09-026-001A-16	Sequence 16, Appl1
35	577.5	12.7	529	2	US-08-836-442-3	Sequence 3, Appl1
36	517	11.4	457	1	US-08-264-101-4	Sequence 4, Appl1
37	517	11.4	457	2	US-08-765-243-4	Sequence 4, Appl1
38	517	11.4	457	5	PCT-US95-07295-4	Sequence 4, Appl1
39	486.5	10.7	439	1	US-09-026-001A-8	Sequence 8, Appl1
40	392	8.6	470	1	US-08-514-014-2	Sequence 2, Appl1
41	392	8.6	470	2	US-08-833-823-2	Sequence 2, Appl1
42	392	8.6	470	3	US-08-813-150-2	Sequence 2, Appl1
43	389.5	8.6	464	4	US-09-411-329C-14	Sequence 14, Appl1
44	387.5	8.5	462	4	US-09-411-329C-3	Sequence 3, Appl1
45	387.5	8.5	462	4	US-09-411-329C-17	Sequence 17, Appl1

ALIGNMENTS

RESULT 1
US-09-351-414-2
Sequence 2, Application US/09351414
Patent No. 6265199
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baird, Nand
APPLICANT: Delisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/351,414
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 696
TYPE: PRT
ORGANISM: Homo sapiens
US-09-351-414-2

Query Match	79.5%	Score 3621:	DB 4:	Length 696:
Best Local Similarity	99.7%	Pred. No. 6.4e-291:		
Matches 654:	Conservative 0:	Mismatches 2:	Indels 0:	Gaps 0:
QY	132	LDTKARHQKHNKAVHLAQAQSFQIEAFSGKFLDILNNGLLSDYVEIHYENCKPQYSK	191	
DB	9	LDTKARHQKHNKAVHLAQAQSFQIEAFSGKFLDILNNGLLSDYVEIHYENCKPQYSK	68	
QY	192	GGEHCYHGSIRGVKDSVVALSTCNGLGHEFDDTFVMIPELVLVHDEKSGRPHITOK	251	
DB	69	GGEHCYHGSIRGVKDSVVALSTCNGLGHEFDDTFVMIPELVLVHDEKSGRPHITOK	128	
QY	252	TIAQOYSKOMNLTMERGDQWFLSELOWLRRKRAVPSPGIFEMMYLEIMYNDHKT	311	
DB	129	TIAQOYSKOMNLTMERGDQWFLSELOWLRRKRAVPSPGIFEMMYLEIMYNDHKT	188	
QY	312	YKRRSSHAHTNFAKSVNLVDSTYKQQLTRVVLVAEFTWETKQDIDITTPVOMLHE	371	
DB	189	YKRRSSHAHTNFAKSVNLVDSTYKQQLTRVVLVAEFTWETKQDIDITTPVOMLHE	248	
QY	372	FSKYRORIKOHADAVHLISRTFHYKRSLSYFSGVCSRTGCVGNEGLPMAVAQVLSQ	431	
DB	249	FSKYRORIKOHADAVHLISRTFHYKRSLSYFSGVCSRTGCVGNEGLPMAVAQVLSQ	308	
QY	432	SLAONLGIOWPSSRRKPKCDCTESWGCIIMETGVSRRKSKCSILEYRPFLOHGGGAC	491	
DB	309	SLAONLGIOWPSSRRKPKCDCTESWGCIIMETGVSRRKSKCSILEYRPFLOHGGGAC	368	
QY	492	LFRPPTKLEPTEGCGNGYVEAGEBDCGFWHECYGLCKCKSLNSGAHCSDBGPCCNNTSC	551	

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DB      369  LENRPRKLEFPEECGGVYEAEECDGCGHVECYGLCKCKCSLSNAGHSDGQCNNITSC 428
QY      552  LFQPRGVECDRAVNECDITEYCTGDSGQCPNHLKODGYACNONOGRVCYNGECKTRDNOC 611
DB      429  LFQPRGVECDRAVNECDITEYCTGDSGQCPNHLKODGYACNONOGRVCYNGECKTRDNOC 488
QY      612  QYIWGTRKAAGSDKFCYEKINTEGTEKNGCKGKDDRMWIOCSKHDPVFCGFLCTNLTRAPRI 671
DB      489  QYIWGTRKAAGSDKFCYEKINTEGTEKNGCKGKDDRMWIOCSKHDPVFCGFLCTNLTRAPRI 548
QY      672  GLOGGIIPTSFYHOGRAVIDCSGAHVLDLDDPDVGVVEGTPCGSPMMLCDRCLIOAL 731
DB      549  GLOGGIIPTSFYHOGRAVIDCSGAHVLDLDDPDVGVVEGTPCGSPMMLCDRCLIOAL 608
QY      732  NMSSCLPDSKGVKSGHGVCSNEATCICDFTWAGTDCSIRDPVRLNHPKDEGPKG 787
DB      609  NMSSCLPDSKGVKSGHGVCSNEATCICDFTWAGTDCSIRDPVRLNHPKDEGPKG 664

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RESULT 2
US-08-243-542-4
: Sequence 4, Application US/08243542
: Patent No. 5552526
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: APPLICANT: EMI, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAs
: TITLE OF INVENTION: ENCODING THE SAME
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
: STREET: 2026 Rambling Road
: CITY: Kalamazoo
: STATE: Michigan
: COUNTRY: USA
: ZIP: 49008-1699
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
: COMPUTER: IBM PC/XT/AT Compatible
: OPERATING SYSTEM: MS-DOS 5.0
: SOFTWARE: WordPerfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/243,542
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-136602
: FILING DATE: 14 MAY 1993
: APPLICATION NUMBER: JP 5-257455
: FILING DATE: 22 SEPTEMBER 1993
: APPLICATION NUMBER: JP 6-49904
: FILING DATE: 23 FEBRUARY 1994
: APPLICATION NUMBER: JP 6-73328
: FILING DATE: 12 APRIL 1994
: APPLICATION NUMBER: JP 6-84470
: FILING DATE: 22 APRIL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Terryence F. Chapman
: REGISTRATION NUMBER: 32 549
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (616) 381-1156
: TELEFAX: (616) 381-5465
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 769 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:

```

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: LIBRARY: human fetal brain cDNA library
: US-08-243-542-4
: Query Match 43.4%; Score 1978; ~DB 1; Length 769;
: Best Local Similarity 48.6%; Pred. No. 5,3e-155;
: Matches 397; Conservative 93; Mismatches 225; Indels 102; Gaps 17;
QY      46  LLLVLLLPPLAASRRRA--WGA----APASPHNNEFAEKNLGLVLAEDDNTLQGNSSS 99
DB      12  LLLSLPPTPLGLTQGPAGALRWGLDQLGGGAP----- 45
QY      100  NISYSNAMOKEITLPSRLIYINODESPYHVLDTFARHQOKHNKAVHLAQAFOLEAFG 159
DB      46  -----EYEPKSLVRE--SSGGEYVRQQLDTRRQEPGPPVHLAQAQVFAFN 94
QY      160  SKFILDILLNGLLSSDYVEIHK--ENCKPOYSKG--GEHCYTHGSIKGVDSKALSTCNG 217
DB      95  SNFTLDLDELNHHLLSSQYVERHFSREGTQSHGAGDHCYQCKLRGNPHSFAALSTCOG 154
QY      218  LHGMFEDDTFYVMIPELELY--HDEKSTGRPHIIOKTLAQYQSKMKNLMEKGDQWPL 275
DB      155  LHGVFSDGNLTLYVEPEVAGPWGAPDGPLILYRT-----PLL 194
QY      276  SELQWLK-----RRKRAVPSRG---IFEMKYLELMIIVNDRKTY 312
DB      195  PDLPGCRPEPCILRAVPAQAPRPNRRLRKRQYR--RGHTVHSEFYVELIYINDQLF 252
QY      313  KHRSSHHTNNFAKSVNLVDSIYKEQLNTRVLVAVEFTERKQIDITTPVOMLHEF 372
DB      253  EOMROSVALTSNFAKSVNLADVIYKEQLNTRVLVAVEFTERKQIDITTPVOMLHEF 312
QY      373  SKYROR-IRQHADAHLISVTFHYKRSLSYFEGVCSFRTGVNVEYGLPMVAQVLSQ 431
DB      313  MYRRREGLPESNATHLFSGRTPQSTSSGAAYVGLCSLHGGGVNTEYGMKGAIAVTLAQ 372
QY      432  SLAONLGTOM-EPSRRPKDCDCTESMGCIMEETGVSHSRKFSKCSILEYRDLQRGGA 490
DB      373  TLGONLGMNKNKRRSSAGDCCKPDIMLCIMEDTGFTLPKRFSKSIDEVNQFLQEGGS 432
QY      491  CLFNRPRLKLEPTEECGGVYEAEECDGCGHVECYGLCKCKCSLSNAGHSDGQCNN 547
DB      433  CLFNRPRLKLEPTEECGGVYEAEECDGCGHVECYGLCKCKCSLSNAGHSDGQCNN 492
QY      548  NTSCLFQPRGVECDRAVNECDITEYCTGDSGQCPNHLKODGYACNONOGRVCYNGE 607
DB      493  R--CYTEPRGVSCREAVNECDIAETCTGDSGQCPNHLKODGYACNONOGRVCYNGE 550
QY      608  DNOCYIWGTRKAAGSDKFCYEKINTEGTEKNGCKGKDDRMWIOCSKHDPVFCGFLCT 667
DB      551  DNOCYIWGTRKAAGSDKFCYEKINTEGTEKNGCKGKDDRMWIOCSKHDPVFCGFLCT 608
QY      668  APRIGLOGLIPTSFYHOGRAVIDCSGAHVLDLDDPDVGVVEGTPCGSPMMLCDRCL 727
DB      609  APRIGLOGLIPTSFYHOGRAVIDCSGAHVLDLDDPDVGVVEGTPCGSPMMLCDRCL 668
QY      728  IQALNMSSCLPDSKGVKSGHGVCSNEATCICDFTWAGTDCSIRDPVRLNHPKDEG 786
DB      669  ASAPNFSTCPGSGERRICSHGVCSNECKCICQDPMWIKGDSIINPLPTSPPTETERY 728
QY      787  GPSATNLIIGSIAGAILVAIVLIGTGNGFNKVR 823
DB      729  GPSATNLIIGSIAGAILVAIVLIGTGNGFNKVR 765

```

```

RESULT 3
US-08-477-407-4
: Sequence 4, Application US/08477407
: Patent No. 5631351
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: APPLICANT: EMI, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAs
: TITLE OF INVENTION: ENCODING THE SAME

```

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243, 542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Teriyence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-477-407-4

Query Match 43.4%; Score 1978; DB 1; Length 769;
Best Local Similarity 48.6%; Pred. No. 5, 3e-155;
Matches 397; Conservative 93; Mismatches 225; Indels 102; Gaps 17;

46 LLLVLLLPPLAASSPRRA--WGA-----AAPSAPHNNEETAENKLVLADEEDNTLQOHSSS 99
12 LLLSLPPGLTGTGPGALRWGCGPQLGPGAP----- 45
100 NISYSNAMOKEITLPSRLIYIYNODESPYHYLDTKARHQKKNKAVHLAQAQSFQIARFG 159
46 -----EYTESRLVRE--SSGGEVAKOOLDTRVROBPFGPPVHLAQVSFVDAFM 94
160 SKFIIDLINNGLLSSDYVEIHY-ENGKPOYSKG-GEHCYHGSINGVDSKVALS:YCNQ 217
95 SNFTLDLELNHLLSSQYVERHFSRGCTQHSYGAGDHCYOGKLGKNGHPSFALS:YCGG 154
218 LHGMEDDTFVYMIRPLELV--HDEKSTGRPHITQTLTLAGQYSKQKNLTMERGDQNPFL 275
155 LHGVSDGDLTYIVEQEVAGPWPAGPQPLPHLYRT-----PLT 194
276 SELQWLK-----RRKRVNPSRG---IPEEMKYLEIMTVNDHKTY 312
195 PPLGCRFEGCLFANVPAQSPAPNRRPLRRKKROYR--RGHPYHSETKYVELIVINDHQLP 252

313 KKRSSHAFNNFNFAKSVVNLVDSIYKQOLNTRVVLVAVENTERKDOIDITTNPYQMLHEF 372
253 EQMROSVVLNFAKSVVNLADVIYKQOLNTRIYLVAMETWADBDKIQVOODLETLARL 312
373 SKYROR-IKOHADAVHLISRTFHYKSSLSYFGVCSRTRGVNEYGLPMAVAQVLSQ 431
313 MYVRREGLPEPSNATHLFSGRTPPOSTSSGAAYVGGICSLSHGGGVNEYGNMGAMAVTLAQ 372
432 SLQONIGIOW-EPSRRPKDCCTESMGCITHEFGVSHSRKFSKSTILEYDFIORGGA 490
373 TLGQNLGMNMMKRRSSAGDCKCPDIWLGCIMEDYGFYLPKRFSSCSIDENYQFLQEGGS 432
491 CLEFRPKLEPTEPCGNGYVAGEECDCGFIVECY---GLCCKKCSLSNGAHCSPCCN 547
433 CLFRPKPLKLDPPRCGNGFVAGEECDCGSVQESBRAGNCKKCTLTLDAMCSDLGCR 492
548 NTSCLFPQPRGYECDVAVNECDITHEYCTGDSGQCPNHLKODGYACNONGRCYNGECKTR 607
493 R--CKYEPRGVSCREAVNECDIAETCTGDSQCPNHLKLDGYCDHEDGRCYGRCKTR 550
608 DNOQYIWTGRKAAGSDKFCYEKLTNTEGTEKNGCKGDKGDRWIOGSKHDVFCGFLCTNLT 667
551 DRQCVLMGHAA--DRCTEKLVEGTERSCCRKSGMWQCSKQDVLGFLLCVNTLS 608
668 APRIGLOGETIIPSYFHOGRVIDCSGAHVVLDDTDTVGYVEDTPCGPMKCLDRKCLQ 727
609 APRIGDLVGDISSYTFYHOGKELDCRGHVLGAGSDLSYEDGTACGPNMLCLDRCLP 668
728 IQALNMSCEPLDSKGYCSHGVCSENEATYICDFTWAGTDCSINDPVANLHP--KDEGPK 786
669 ASAFNFSTCPGSGGERRICSHHGVCSENEKCIQCPDMWCKDCSINHLPTSPPTGETERYK 728
787 GPSATNLIISAGAILVAALVILGTMGFWGNVKKR 823
729 GPSGTNIIIGSIAGVLAALVILGTMGFWGNVKKR 765

RESULT 4

US-08-484-355-4:

Sequence 4, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
TITLE OF INVENTION: MDC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484, 355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243, 542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328

FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-484-355-4

Query Match 43.4%; Score 1978; DB 1; Length 769;

Best Local Similarity 48.6%; Pred. No. 5,3e-155;
Matches 397; Conservative 93; Mismatches 225; Indels 102; Gaps 17;

46 LLLVLLLPPLAASSRRA--WGA---AAPSAPHWNETAEKNLGLVADEDNLTLOQSSS 99
12 LLLSLPTPLGTGCPAGALRWGGLPOLGPGAP----- 45
100 NISYSAMKETTIPRLIYINODESEYHVDTCARHQKINKAVHLAQAFOIEARG 159
46 -----EYEPRLVRE--SSGEVRKQQLDITVROEPPGPGPVHLAQAQSEVPAFN 94
160 SKFIIDLINGLSSDYVEIHY--ENGKPOYSKG--GEHCYHGSIRGVKSKYALSTCNG 217
95 SNFTDLLELHLLSSQYVERHRSREGTQHSAGADHCYQGLKNGNPSFALSTCQ 154
218 LHMFPDDTFVYIIELELY--HDEKSTGRPHIIOKTLAQAQYSKOMKMLTMEGDMPL 275
155 LHGVFSDGNLIYIVEPOEYAGPWGAPQGLPHLIYRT-----PLL 194
276 SELQWLK-----RRKRAVNPGRG---IPEKKYLELMIYNDHKTY 312
195 PDLGREGGCLFAVAQAAPRPRRLRRKROYR--RGHPTVSEIKYVLLIYINDHQL 252
313 KHRSSHHTNNEFAKSVNLVDSIYKEQLNTRVLAVAETWTEKQDITITNPVOMLHEF 372
253 EQMROSVLTSNFAKSVNLADVIYKEQLNTRIVLAMETWADGDKIOVODDLETLARL 312
373 SKYROR--IQOHDAVILISRVPHYKRSLSYFGVCSRTRGVGVNVEYGLPMAVAQVLSQ 431
313 MYRRRGLEPSPNATLFGSRTFOSTSSGAAYVGICSLSHGGVNEYGMGMAAYTLAQ 372
432 SLAONLGIOM--EPSSRRPKCDCTESWGCI MEETGSHSRKFSKSTLEFRDLORRGA 490
373 TLGONLGMAMNKRHSAGDCKPDILGCI MEETGFLPRKFSRCSIDEINQLOREGGS 432
491 CLFNRPYKLEPTECGNGIYAGEECDCGFHVECY---GLCKCKSLNSAHCSDGPCN 547
433 CLFNKPLKLLDPECCNGFEAGEECDCGVSQCSRAAGCKCKTLLHDAMSDGICCR 492
548 NTSCLPQPGIYECRDVAVNECDITEYCTGDSGQCPRLNHRQDYACNORCNGECKTR 607
493 R--CKTEPRVSCREAVNECDIAETCTGDSQCPRLNHRKIDGYICDHEGRCYGGRCR 550
608 DNOCQYIMGTAKAGSKFCYEKINTEGTEKNGCKGDQRMILQCSKHDVFGFLCTMLTR 667
551 DRCCQYLMGMAA--DRFCYEKLINTEGTEKNGSGCRKSGVQCSKQDVLGFLICVINS 608
668 APRIGOLGEIITFTSYHOGRIYDCSGAHVYLDLDDTVGVYEDGTGCGPSMCLDRKCLQ 727
609 APRIGDLVGDSSVTFYHOGKEIDRCGHVQLADGSDLSVEVDGTACGPMMLCIDHRCPL 668

QY 728 IQALNMSQPLDSKGVCSGHGVCSENEATCIDFTWAGTDCSTIRDEVNRLHP--KDEGPK 786
Db 669 ASAFNFTSTCPGSEERRICSHHGVCSNECKICOPDWTGKDCSTHNDLPTSPPTGETERYK 728
QY 787 GPSATMLIIGTAGALVAIAIVLGIGTGWGFKNVKKRR 823
Db 729 GPSGTMIIGTAGAVLAIAIVLGIGTGWGFKNIRRR 765

RESULT 5

US-08-243-542-3

Sequence 3, Application US/08243542

Patent No. 5532526

GENERAL INFORMATION:

APPLICANT: NAKAMURA, YOSUKE

APPLICANT: EMI, MITSURU

TITLE OF INVENTION: MDC PROTEINS AND DNAs

TITLE OF INVENTION: ENCODING THE SAME

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.

STREET: 2026 Rambling Road

CITY: Kalamazoo

STATE: Michigan

COUNTRY: USA

ZIP: 49008-1699

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 MB storage

COMPUTER: IBM PC/XT/AT Compatible

OPERATING SYSTEM: MS-DOS 5.0

SOFTWARE: Wordperfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/243,542

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-136602

FILING DATE: 14 MAY 1993

APPLICATION NUMBER: JP 5-257455

FILING DATE: 22 SEPTEMBER 1993

APPLICATION NUMBER: JP 6-49904

FILING DATE: 23 FEBRUARY 1994

APPLICATION NUMBER: JP 6-73328

FILING DATE: 12 APRIL 1994

APPLICATION NUMBER: JP 6-84470

FILING DATE: 22 APRIL 1994

ATTORNEY/AGENT INFORMATION:

NAME: Terrence F. Chapman

REGISTRATION NUMBER: 32 549

REFERENCE/DOCKET NUMBER: Furuya Case 1313

TELECOMMUNICATION INFORMATION:

TELEPHONE: (616) 381-1156

TELEFAX: (616) 381-5465

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 670 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

LIBRARY: human fetal brain cDNA library

US-08-243-542-3

Query Match 41.0%; Score 1867.5; DB 1; Length 670;

Best Local Similarity 51.8%; Pred. No. 6e-146;
Matches 357; Conservative 89; Mismatches 184; Indels 59; Gaps 13;

QY 168 LNNGLSSDYVEIHY--ENGKPOYSKG--GEHCYHGSIRGVKDSVVALSTCNGLHMFEDD 225
Db 4 LSHLLSSQYVERHRSREGTQHSAGADHCYQGLKNGNPSFALSTCQGLHGVESDG 63

Db 518 GDISSVTFYHQKELDCRGHVOLADSDLSYVEDGTACGPNMLCDHRCLPASAFNFST 577
OY 736 CPLDSKRGVSGHGVCSNEATCICDFTWAGTDCSIRDPVRNLHP-KDEGFKGSAITLI 794
Db 578 CPGSGERRICSHHGVCSNEKCIQCPDWTGKDCSIHNLPTSPPTGETERYKGPSTINII 637
OY 795 IGSTAGAILVAIYVIGTGWGFKNVKRR 823
Db 638 IGSTAGAILVAIYVIGTGWGFKNIRGR 666

RESULT 7
US-08-484-355-3
Sequence 3, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Teriyence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furiya Case 1313
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-484-355-3

Query Match 41.0%; Score 1867.5; DB 1; Length 670;
Best Local Similarity 51.8%; Pred. No. 6e-146;
Matches 357; Conservative 89; Mismatches 184; Indels 59; Gaps 13;

OY 168 INNGLLSSDYVEIHY-ENGKPOYSKG-GEHCYHSGISIRGVKDSKVALSTCNGLHGFEDD 225
Db 4 LSHOLLSSQYVERHRSRECTTOHSTGAGDHCYQCKLRGNPHSFAALSTYCGGLHGVFSG 63
OY 226 TFVYMIIEPLV--HDEKSTGRPHIIQKTLAQOYSQNMKNLMEMRGDDQPFISELOMK- 282
Db 64 NLTYIVEPOEVAGPMGADQGPLPHLYRT-----PLLPDLPGCE 103
OY 283 -----RRKRAVNSRG-----IFEEMKYLEIMTVNDKRYKKHSSHA 320
Db 104 PCCLFAVPAQASAPPNRPLRRKRQV--RGHPVHSETVVELIIVNDHQLEFQMSQVY 161
OY 321 HTNNEFAKSVNLDVSIYKQOLNTRVYLVAVETWTEKDQIDITNPVQMLHESKYQR-1 379
Db 162 LTSNFAKSVNLDVSIYKQOLNTRVYLVAVETWADDKIOVODDLETLARLVYRREGI 221
OY 380 KOHDAVHLISRTFHYKRSLSYFGVCSRTGCVNVEGLPMVAVOYLSSLOALNGI 439
Db 222 PEPSNATHLFSGRTFPOSTSSGAAYVGGTSLSHGGVNETGNMGAMAVYLAOTLQONLGM 281
OY 440 QW-EPSSRRPKDCTESMGCI MEETGVSHSRKFSKSILEYRDLQORGAGCLFNRPTK 498
Db 282 MNKHSSAGDCKCPDMLNLCIMEDIGFYLPKRFKSIDEVNOFQEGGSGCLFNKPLK 341
OY 499 LFEPTCGNGYVAGEGDCGFHVECY---GLCKKCSLSNGARCSGPPCCNNTSCLFOP 555
Db 342 LLDPECGNGFYVAGEGDCGVSQESRAAGNCKCKCTLTHDAMCSGDLCCR--CYEP 399
OY 556 RGEYCRDAVNECOTTECTGDSGCPNLLKODGYACNOGNRYNECKTRPDQCOYIW 615
Db 400 RGVSCRAVNECDIAECTGDSGCPNLLKODGYACNOGNRYNECKTRPDQCOYIW 459
OY 616 GTKAGSDKFCYEKLTEGTEKNGCGKDGDRWIDQSKHDFEGFLLCTNLTAPRIGOLQ 675
Db 460 GHAA--DRCYELNTEGTERGSCGRKGSAMVOCSDOVLGRLLCVINISGARLIDL 517
OY 676 GEIIPTSFYHQKELDCRGHVOLADSDLSYVEDGTACGPNMLCDHRCLPASAFNFST 577
Db 518 GDISSVTFYHQKELDCRGHVOLADSDLSYVEDGTACGPNMLCDHRCLPASAFNFST 577
OY 736 CPLDSKRGVSGHGVCSNEATCICDFTWAGTDCSIRDPVRNLHP-KDEGFKGSAITLI 794
Db 578 CPGSGERRICSHHGVCSNEKCIQCPDWTGKDCSIHNLPTSPPTGETERYKGPSTINII 637
OY 795 IGSTAGAILVAIYVIGTGWGFKNVKRR 823
Db 638 IGSTAGAILVAIYVIGTGWGFKNIRGR 666

RESULT 8
US-08-243-542-2
Sequence 2, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542

FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-243-342-2.

Query Match 28.5%; Score 1297; DB 1; Length 524;
Best Local Similarity 49.5%; Pred. No. 6.2e-99;
Matches 256; Conservative 65; Mismatches 138; Indels 58; Gaps 12;
168 LNLGLSSDYVEIYH-ENGKPOYSKG-GEHCYHGSIRGVKDSKVALSTCGLHGFEDD 225
4 LSHOLLSSQYVERHFSREGTTOHSTGAGDHCYOGKLRGNPHSFALSTCGLHGFESDG 63
226 TFWYMIPELELV--HDEKSTGRPHIIOKTLAQSOKMKNLMBRQDQWFLSELQMLK- 282
64 NLTYIVEPQVAVGAPGAPGRPLPLIYRT-----PLPDPPLGCRE 103
293 -----RRKRAVNPSSRG---IFEEMKYLEIMIVNDHKTYKKHRS SHA 320
104 PGCLFAVPAQASAPRPNRLRRKROVR--RGHPTVHSETKYVELIVINDHOLFQDMOSV 161
321 HTNNAKSVNLVDSITYKEQLTRVYLAVALVETWTEKQDIDITTPVOMLHEFSKYRGR-1 379
162 LTSNFAKSVNLVADIVYKEQLTRIVLVALETWADGDKIQVODDLETLARLVYRRREG 221
380 KOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVGVNXYGLPMVAQVLSOSLQNLGI 439
222 PEPNATLHLSGRTQOSTSSGAAIVGGICLSHGGVNVYGMNMAVTLAOTLQNLGM 281
440 QW-EPSRKPCKDCTESWGCGIMEETGVSHSRKFSKCSILEYRDLORGGACLEFMRPTK 498
282 MNKHRSSAGDCKPCDINLGMICMEDTGYFLPRKFSKCSIDELYNQLOEGSGSLFKPKPLK 341
499 LPEPECGNGYVEAGEEDCCGHVVCY---GLCKKCSLSNGAHSGDGCPCNNTSCLFOP 555
342 LLDPEPCNGVEAGEEDCCGVSQCSFRAGCNCKKCTLTTHAMCSGLCCRR--CKYEP 399
556 RGYEGRDVAIVEDITCYCTGDSGCGCPNHLKQDGYACNNOGRVYNGEKTGNDNOQYIM 615
400 RGVSRERAVNECDIAETCTGDSGCGCPNHLKQDGYACNNOGRVYNGEKTGNDNOQYIM 459
616 GTKAAGSDKFCYEKLNTEKTEKNGCKGDWRNTOCS 652
460 CHAA--DRFCYEKLNTEKTEKNGCKGDWRNTOCS 494

RESULT 9
US-08-477-407-2
Sequence 2, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
City: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-477-407-2
Query Match 28.5%; Score 1297; DB 1; Length 524;
Best Local Similarity 49.5%; Pred. No. 6.2e-99;
Matches 256; Conservative 65; Mismatches 138; Indels 58; Gaps 12;
168 LNLGLSSDYVEIYH-ENGKPOYSKG-GEHCYHGSIRGVKDSKVALSTCGLHGFEDD 225
4 LSHOLLSSQYVERHFSREGTTOHSTGAGDHCYOGKLRGNPHSFALSTCGLHGFESDG 63
226 TFWYMIPELELV--HDEKSTGRPHIIOKTLAQSOKMKNLMBRQDQWFLSELQMLK- 282
64 NLTYIVEPQVAVGAPGAPGRPLPLIYRT-----PLPDPPLGCRE 103
293 -----RRKRAVNPSSRG---IFEEMKYLEIMIVNDHKTYKKHRS SHA 320
104 PGCLFAVPAQASAPRPNRLRRKROVR--RGHPTVHSETKYVELIVINDHOLFQDMOSV 161

OY		321	HTNNFAKSVNLDISTYKEQDNTNVVLVAVETWEMXKDIDITFTNVVOJHEFSKROR-I	379
			. : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :	
Db		162	LTSNFAPSVNLADVIYIKEDQENTRILVAMETWAGDKIQOODDLLETLARLMVTRREL	221
OY		380	KOHDAVHLISRVFHFHYKRSSLFEVGVCSTRGVAVNEGLPMAVAQVLSOSLAONLGI	439
			: : : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :	
Db		222	PEPSNAHLLHSGRFFQSTSSGANAUYGLCSLSHGSGVADEYMGMMGAAVYLTAQTGGNLM	281
OY		440	QW-EPSSRRPKCDCTESMGCIMETEGVSHSKFKSCSILEYRDLQRGGACLFNRPK	498
			. : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :	
Db		282	MMNHRSASAGCKCPDIMLGCI MEDTGYLPKFRSCSIDENYOFLQEBGGSCFLFNKPPLK	341
OY		499	LEPTECGNGYVEAGEECDCGFHVICY---GLCCKKCSLSNAGHCSDSPCUNNTSOLFOP	555
			. : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :	
Db		342	LIDPRECCNGEYVEAGEBCDCGSVOEC SRAGCGCKCTLTHAMCSDGLCCR--CRYEP	399
OY		556	RGYEGRDVAVNDDITREYCTGDSGDGPBPMLHKODGVACNONOGRCYNGSEKTRPDNOQIYW	615
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OY		616	GTKAAGSDFCYEKLNTGEKGCGCKDGDRWIQCS	652
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RESULT 10
 US-08-484-355-2
 Sequence 2, Application US/08484355
 Patent No. 5705341
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, YUSUKE
 APPLICANT: EMI, MITSURU
 TITLE OF INVENTION: MDC PROTEINS AND DNAS
 TITLE OF INVENTION: ENCODING THE SAME
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLYNN, THEIL, BOTTELL & TANIS P.C.
 STREET: 2026 Rambling Road
 CITY: Kalamazoo
 STATE: Michigan
 COUNTRY: USA
 ZIP: 49008-1699
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
 COMPUTER: IBM PC/XT/AT Compatible
 OPERATING SYSTEM: MS-DOS 5.0
 SOFTWARE: wordperfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,355
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/243,542
 FILING DATE: 13-MAY-1994
 APPLICATION NUMBER: JP 5-136602
 FILING DATE: 14 MAY 1993
 APPLICATION NUMBER: JP 5-257455
 FILING DATE: 22 SEPTEMBER 1993
 APPLICATION NUMBER: JP 6-49904
 FILING DATE: 23 FEBRUARY 1994
 APPLICATION NUMBER: JP 6-73328
 FILING DATE: 12 APRIL 1994
 APPLICATION NUMBER: JP 6-84470
 FILING DATE: 22 APRIL 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Terryence F. Chapman
 REGISTRATION NUMBER: 32 549
 REFERENCE/DOCKET NUMBER: Furuya Case 1313
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (616) 381-1156
 TELEFAX: (616) 381-5465
 INFORMATION FOR SEQ ID NO: 2:

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?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 524 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? IMMEDIATE SOURCE:
? LIBRARY: human fetal brain cDNA library
? JS-08-484-355-2

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Query Match	28.5%	Score 1297	DB 1	Length 524
Best Local Similarity	49.5%	Pred. No. 6.2e-99		
Matches 256	Conservative 65	Mismatches 138	Indels 58	Gaps 12

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QY      168  ANNGLSDDYAEIHH - ENKRPQYS-GG - GECYHHSIGVNDKSYALSTCNDLHMFEJD 222
Db      4    LSHOLLSSQYVERHFSRECTQIHOHSTGADHCHCYQOGLKNGPNHSPALSTCQGLHCVFSDG 63
QY      226  TFVYVIEBLELV - HDEKSTGRPHIIIOKTLAGQYSKOKNLTWEGDOPFLSELOMUK - 282
Db      64  NLTYTEVEQEVAGPWGAPFOGRLPHLYRP - -----PLLPDLCRE 103
QY      283  -----RRKRAVNPSSG---IFEEMKYTELMTIVNDKHYTKRKHSSHA 320
Db      104  PEGLEFAVPAQSAAPRNRPRLRRKKROYR - -RGHTVHSETKYTELVIIINDQLEPQOMROSVV 161
QY      321  HTNNFAKSVYNLVDSIYKEQLNTRVYLVAVEFTWEEKDQIDITTNPOMLHESKYRQR -I 379
Db      162  LTSNFAKSVYNLADVLYKKEQLNTRVYLVAMETWADKLOVODDDLETLARLAMYRREGI 221
QY      380  KOHAUAVHILSVYTFPHYKRSSLSEFGGVSRTRGVAVNEVEGSLPMAVAQVLSOSIAONLGI 439
Db      222  PEPNSNATHLFSGRTQIOTJSSGAAYVGGICLSIHGGGVNEXGNNMGAMAVTLAOTLGNLGN 281
QY      440  QW - EBSRRPKDCDCTESWGCCTMEETGVSHSRKFSKCSILLEYEDLORGGALLENRPK 498
Db      282  MNKKHRRSSSGDCKPCPDIMGLGIMEDRGFYLPKRFKSCSIDENQFLOJEGGSGLEFNKPLK 341
QY      499  LFEPTRCGAGYVAGEEGECDCGFIVECY ---GLCCRKCSLSNGAHSCDSPCCNNTSCLFOP 555
Db      342  LLDPEPCGNGFYVAGEECDGGSQVDECSBRAGNCCNCKCTLHNDAMCSGLCCRR - -CKYEP 399
QY      556  RGYECDAYNECDITEYCTGDSSQCCPRLHKDQGIACNQNQSGCYNGECTRNDQOQYIW 615
Db      400  RGVSCREAVNECDIAETCTGDSSQCCPRLHKDQYICDHDQGRCYGGKCTKRDQOCVLM 459
QY      616  GTFAAGSDKRCYCEKLTNEGTEKNGNCGDGGRWIIOCSK 652
Db      460  GHAAA - DRCTYKLVNVEGTERSGCGKKGSGWVQCSK 494

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RESULT 11
 US-08-243-542-1
 Sequence 1, Application US/08243542
 Patent No. 5552526
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, YUSUKE
 APPLICANT: EMI, MITSURU
 TITLE OF INVENTION: MDC PROTEINS AND DNAS
 TITLE OF INVENTION: ENCODING THE SAME
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FIVNN, THEIEL, BOUTELL & TANIS P.C.
 STREET: 2026 Rambling Road
 CITY: Kalamazoo
 STATE: Michigan
 COUNTRY: USA
 ZIP: 49008-1699
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inches, 1.44 MB storage
 COMPUTER: IBM PC/XT/AT Compatible
 OPERATING SYSTEM: MS-DOS 5.0

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2003, 18:30:26 ; Search time 128 Seconds
(without alignments)
657.954 Million cell updates/sec

Title: US-09-634-252a-4
Perfect score: 4553
Sequence: 1 MKPPGSSRROPPLAGCSLAG.....GWFKNVKKRRDPDTPQGP 832

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4553	100.0	832	US-09-824-129-3	Sequence 3, Appl 1
2	3621	79.5	696	US-09-809-790-2	Sequence 2, Appl 1
3	3621	79.5	696	US-09-809-617-2	Sequence 2, Appl 1
4	1680	36.9	540	US-09-792-2008-18	Sequence 18, Appl 1
5	1007.5	22.1	778	US-10-125-470-16	Sequence 16, Appl 1
6	1007.5	22.1	778	US-10-125-452-16	Sequence 16, Appl 1
7	1007.5	22.1	778	US-09-955-504-16	Sequence 16, Appl 1
8	1007.5	22.1	918	US-10-020-733-4	Sequence 4, Appl 1
9	1007.5	22.1	918	US-10-125-470-9	Sequence 9, Appl 1
10	1007.5	22.1	918	US-10-125-452-9	Sequence 9, Appl 1
11	1007.5	22.1	918	US-09-955-504-9	Sequence 9, Appl 1
12	1007.5	22.1	926	US-10-020-733-2	Sequence 2, Appl 1
13	1007.5	22.1	955	US-10-020-733-8	Sequence 8, Appl 1
14	1007.5	22.1	963	US-10-020-733-6	Sequence 6, Appl 1
15	982	21.6	920	US-09-792-2008-16	Sequence 16, Appl 1
16	968	21.3	920	US-09-983-531A-4	Sequence 4, Appl 1
17	966	21.2	903	US-09-983-531A-2	Sequence 2, Appl 1
18	962.5	21.1	735	US-09-978-192A-74	Sequence 74, Appl 1
19	962.5	21.1	735	US-09-978-697-74	Sequence 74, Appl 1

20	962.5	21.1	735	US-09-978-192A-74	Sequence 74, Appl 1
21	962.5	21.1	735	US-09-999-832A-74	Sequence 74, Appl 1
22	962.5	21.1	735	US-09-978-189-74	Sequence 74, Appl 1
23	962.5	21.1	735	US-10-174-590-88	Sequence 88, Appl 1
24	962.5	21.1	735	US-10-176-758-88	Sequence 88, Appl 1
25	962.5	21.1	735	US-10-175-737-88	Sequence 88, Appl 1
26	962.5	21.1	735	US-10-173-706-88	Sequence 88, Appl 1
27	962.5	21.1	735	US-10-175-738-88	Sequence 88, Appl 1
28	962.5	21.1	735	US-10-175-752-88	Sequence 88, Appl 1
29	962.5	21.1	735	US-10-176-482-88	Sequence 88, Appl 1
30	962.5	21.1	735	US-10-176-757-88	Sequence 88, Appl 1
31	962.5	21.1	735	US-10-176-913-88	Sequence 88, Appl 1
32	962.5	21.1	735	US-10-180-552-88	Sequence 88, Appl 1
33	962.5	21.1	735	US-10-180-557-88	Sequence 88, Appl 1
34	962.5	21.1	735	US-10-173-700-88	Sequence 88, Appl 1
35	962.5	21.1	735	US-10-174-572-88	Sequence 88, Appl 1
36	962.5	21.1	735	US-10-174-579-88	Sequence 88, Appl 1
37	962.5	21.1	735	US-10-174-582-88	Sequence 88, Appl 1
38	962.5	21.1	735	US-10-174-588-88	Sequence 88, Appl 1
39	962.5	21.1	735	US-10-175-739-88	Sequence 88, Appl 1
40	962.5	21.1	735	US-10-175-740-88	Sequence 88, Appl 1
41	962.5	21.1	735	US-10-176-488-88	Sequence 88, Appl 1
42	962.5	21.1	735	US-10-176-492-88	Sequence 88, Appl 1
43	962.5	21.1	735	US-10-176-747-88	Sequence 88, Appl 1
44	962.5	21.1	735	US-10-176-750-88	Sequence 88, Appl 1
45	962.5	21.1	735	US-10-176-750-88	Sequence 88, Appl 1

ALIGNMENTS

RESULT 1
US-09-824-129-3
Sequence 3, Application US/09824129
Patent No. US2002001840A1
GENERAL INFORMATION:
APPLICANT: Lopez-Otin, Carlos
APPLICANT: Miguel, Santiago Cal
APPLICANT: Freije, Jose Maria Perez
APPLICANT: Garcia, Jose Manuel Lopez
APPLICANT: Bianchi, Albert Bernard
APPLICANT: Trill, Pamela
TITLE OF INVENTION: Methods and Compositions for Modulating
Integrin-mediated Cell-Cell Interactions
FILE REFERENCE: D0015-NP
CURRENT APPLICATION NUMBER: US/09/824,129
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/194,164
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
US-09-824-129-3
Query Match 100.0%; Score 4553; DB 10; Length 832;
Best Local Similarity 100.0%; Pred. No. 9, 6e-301;
Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPPGSSRROPPLAGCSLAGSCGPGAGVPASAPARTPPCRLLVLLPLPLAAS 60
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DB 1 MKPPGSSRROPPLAGCSLAGSCGPGAGVPASAPARTPPCRLLVLLPLPLAAS 60
|||||
QY 61 RPRAMGAAPASAPAHMETAEKNLGVLADEDNTLQONSSNITSYNNMQKEITLPSRLIY 120
|||||
DB 61 RPRAMGAAPASAPAHMETAEKNLGVLADEDNTLQONSSNITSYNNMQKEITLPSRLIY 120
|||||
QY 121 INDDSPPHVLDTKRHHQKHKAVHQAASQIEAFSGKFTLLDILNGLSSDYVEI 180
|||||
DB 121 INDDSPPHVLDTKRHHQKHKAVHQAASQIEAFSGKFTLLDILNGLSSDYVEI 180
|||||

QY 181 HYENKGPQYSGGHEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVEHDE 240
DB 181 HYENKGPQYSGGHEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVEHDE 240
QY 241 KSTGRPHIIOKTLAAGYSGKQKMLTMRGDQWPLSELQWLKRRRAVNSRGIFEEMKY 300
DB 241 KSTGRPHIIOKTLAAGYSGKQKMLTMRGDQWPLSELQWLKRRRAVNSRGIFEEMKY 300
QY 301 LELMIVDHTYKRRSHHTNNFAKSVNLVDSIYKEQINTRVYLAVETWEKQID 360
DB 301 LELMIVDHTYKRRSHHTNNFAKSVNLVDSIYKEQINTRVYLAVETWEKQID 360
QY 361 ITTNPVOMLHEFSKRYRORIKOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVNEYG 420
DB 361 ITTNPVOMLHEFSKRYRORIKOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVNEYG 420
QY 421 LPMVAOVLSOSIAONLGIQWEPSSRRPKCDCTESWGGCIMEETGVSHSRKFSKSILEY 480
DB 421 LPMVAOVLSOSIAONLGIQWEPSSRRPKCDCTESWGGCIMEETGVSHSRKFSKSILEY 480
QY 481 RDELQGGAGACLFNRPDKLEPTECGNGYVAGEECCGPFHVECYGLCKKCSLSNGAHC 540
DB 481 RDELQGGAGACLFNRPDKLEPTECGNGYVAGEECCGPFHVECYGLCKKCSLSNGAHC 540
QY 541 SDBPCNNNSCLTQPPRGYECRDVNECDITEYCTGDSGQCPNHLKODGYACNONGRCY 600
DB 541 SDBPCNNNSCLTQPPRGYECRDVNECDITEYCTGDSGQCPNHLKODGYACNONGRCY 600
QY 601 NGECCKTRDNOCCOYIMGTAKAGSDKFCYEKLTNTEGTEKNGCKDGRMIOCSKHDFVCGFL 660
DB 601 NGECCKTRDNOCCOYIMGTAKAGSDKFCYEKLTNTEGTEKNGCKDGRMIOCSKHDFVCGFL 660
QY 661 LCTNLTFRAPRIGOLGEEIIPTSFYHOGRAVIDCSGAHVLLDDDTDVGVEDEGTFCGFSMNC 720
DB 661 LCTNLTFRAPRIGOLGEEIIPTSFYHOGRAVIDCSGAHVLLDDDTDVGVEDEGTFCGFSMNC 720
QY 721 LBRKCIQIALNNSCPLDSKGVCSGHVCSNEATCICDFTYAGTDCSIRDPVRLNHP 780
DB 721 LBRKCIQIALNNSCPLDSKGVCSGHVCSNEATCICDFTYAGTDCSIRDPVRLNHP 780
QY 781 KDEGPKGPSATNLIGSISAGAILVAIVLGTGTGKFNKKRRFDPFGOQPI 832
DB 781 KDEGPKGPSATNLIGSISAGAILVAIVLGTGTGKFNKKRRFDPFGOQPI 832

RESULT 2
US-09-809-790-2
; Sequence 2, Application US/09809790
; Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Delisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-790-2

Query Match 79.5%; Score 3621; DB 10; Length 696;
Best Local Similarity 99.7%; Pred. No. 1.3e-237;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 132 LDTKARHQQKHNKAVHLAQSFOIEAFGSKFLIDLINNGLLSSDYVEIHYENKGPQYK 191

DB 9 LDTKARHQQKHNKAVHLAQSFOIEAFGSKFLIDLINNGLLSSDYVEIHYENKGPQYK 68
QY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVEHDEKSTGRPHIIOK 251
DB 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVEHDEKSTGRPHIIOK 128
QY 252 TLGAQYSGKQKMLTMRGDQWPLSELQWLKRRRAVNSRGIFEEMKYLELMIVDHT 311
DB 129 TLGAQYSGKQKMLTMRGDQWPLSELQWLKRRRAVNSRGIFEEMKYLELMIVDHT 188
QY 312 YKRRSHHTNNFAKSVNLVDSIYKEQINTRVYLAVETWEKQIDITTNPVOMLHE 371
DB 189 YKRRSHHTNNFAKSVNLVDSIYKEQINTRVYLAVETWEKQIDITTNPVOMLHE 248
QY 372 FSKYRORIKOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVNEYGLPMVAOVLSQ 431
DB 249 FSKYRORIKOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVNEYGLPMVAOVLSQ 308
QY 432 SLAONLGIQWEPSSRRPKCDCTESWGGCIMEETGVSHSRKFSKSILEYRDELQGGAG 491
DB 309 SLAONLGIQWEPSSRRPKCDCTESWGGCIMEETGVSHSRKFSKSILEYRDELQGGAG 368
QY 492 LFNRPDKLEPTECGNGYVAGEECCGPFHVECYGLCKKCSLSNGAHCSDGFCNNNTSC 551
DB 369 LFNRPDKLEPTECGNGYVAGEECCGPFHVECYGLCKKCSLSNGAHCSDGFCNNNTSC 428
QY 552 LFQPRGYECRDVNECDITEYCTGDSGQCPNHLKODGYACNONGRCYNGECCKTRDNO 611
DB 429 LFQPRGYECRDVNECDITEYCTGDSGQCPNHLKODGYACNONGRCYNGECCKTRDNO 488
QY 612 OYIMGTAKAGSDKFCYEKLTNTEGTEKNGCKDGRMIOCSKHDFVCGFLCTNLTFRAPR 671
DB 489 OYIMGTAKAGSDKFCYEKLTNTEGTEKNGCKDGRMIOCSKHDFVCGFLCTNLTFRAPR 548
QY 672 GOLGEEIIPTSFYHOGRAVIDCSGAHVLLDDDTDVGVEDEGTFCGFSMNCIDRKCLOIAL 731
DB 549 GOLGEEIIPTSFYHOGRAVIDCSGAHVLLDDDTDVGVEDEGTFCGFSMNCIDRKCLOIAL 608
QY 732 NMSSCPLDSKGVCSGHVCSNEATCICDFTYAGTDCSIRDPVRLNHPKDEGPKG 787
DB 609 NMSSCPLDSKGVCSGHVCSNEATCICDFTYAGTDCSIRDPVRLNHPKDEGPKG 664

RESULT 3
US-09-809-617-2
; Sequence 2, Application US/09809617
; Patent No. US20020137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Delisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-617-2

Query Match 79.5%; Score 3621; DB 10; Length 696;
Best Local Similarity 99.7%; Pred. No. 1.3e-237;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 133 LDTKARHQQKHNKAVHLAQSFOIEAFGSKFLIDLINNGLLSSDYVEIHYENKGPQYK 191

Db 237 LIETANYDKFYR-SLNIIRIALVGLVWTHGNMCEVSENPYSTLWSFLSWRRKLLAOKYH 295
OY 384 DAVHLISRYTFPHYKRSLSYFGVCS--RTRGVVNEGYELPMVAVOYLSOSLAONLGIOW 441
Db 296 DNAQLITGMSPHGTTIGLAPLMAVCVYOSGVNMDHSENAIGVATMTAHEMGNHGMTH 355
OY 442 EPSSRRKPKDCTESWGCIM-EETGVSHSRKFSKSILEYRDLORGACLEFNR--TK 498
Db 356 DSAD--CCSASADGGCIMAATGHPFKVFNCGNRRLDRLYLOSOGGMCLSNMPDTRM 412
OY 499 LEFTEECNGYVAGEECDCGFHVECYGLCC--KKCSLSNGAHGSDGPCNNNTSCLFQPR 556
Db 413 LVGGRGNGYLEDGEEDCCGEECCNPNCCNASNCTLRPGAECAGHSCCH--QCKLLAP 470
OY 557 GYECDAVNECDITEYCTGDSGCCPPLHKODGYACNONGRCYAGECKTRNOCQYIWG 616
Db 471 GTLCREQARQCDLPECTGKSPHCPTNFYOMDGTCEGQAYCYNMCLITYOEQOQOLMG 530
OY 617 TRAAISDRFCYKLTBEGTEKNGCKD-GDRWIOGSKHDVFCGLTCTNLTRAPRIGOLQ 675
Db 531 PGARPAIDICEKVNAGDITFGNCGKDMNGEHRKCMRDAKCGKIQOCSSEAR--LE 586
OY 676 GEIIP--TSFYHOGVYIDCSGAHVYL----DDOTDVGVEDGTFCGSPSMCLDRKCLQI 728
Db 587 SNAVIDITTIMNGROIQRGTHYRGPEEGDMLPELVMTGKXGNHICFEQOCNRT 646
OY 729 QALNMSCPDLSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKGP 788
Db 647 SFEETEGC-----GKCKNGHGVCCNNONCHCLPGMAPFCNTPGHGSII-----DSGPMPP 697
OY 789 SATNLIIGSINGAILVAIVL 809
Db 698 ESVGPVAVGVLVAILVAILM 718

RESULT 6
US-10-125-452-16
Sequence 16, Application US/10125452
Patent No. US20020173640A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE REFERENCE: PTO06P2
CURRENT APPLICATION NUMBER: US/10/125,452
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/955,504
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 09/712,907
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: PCT/US00/14308
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/178,717
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/142,930
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/136,388
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 778
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-452-16

Query Match 22.1%; Score 1007.5; DB 9; Length 778;
Best Local Similarity 31.5%; Pred. No. 31e-60;
Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

OY 38 PARTPCRLVLLPLPLAASRRPANGAAPSAPHNNETAENKVLGLADEDNLTQONS 97
Db 2 PEGAGAAARCLLAFALQPL--RPR-----AAREPGMTRSEEB----- 37

OY 98 SSNISYSNAMOKEITLPSRLIYIYNODESPYHVLDTKARHQQHNKAVHLAQSFOLEA 157
Db 38 -----SPKQLHELIIPW-----KTISESY-----REKHPKALVYMA 71
OY 158 FGSKIIDLILNLGLSSDYVEIHV-ENGKPOYS--KGECHYHGSIRGVKDSKVALST 214
Db 72 EGRELIDLEKNEDLFAPSYETETHYSSGNQOTTRKLEDCHFHGVIRELSSVTLST 131
OY 215 CNGLHGMFE-DOTFVYMEPELHVHDEKSTGRPHILIKTLAOGYSKQMK-----NLWERG 269
Db 132 CRGIRGLTIVSSNLSTYIEPLP--DSKG--QHLYR-----SEHLKPPGCGFEHS 179
OY 270 D-----QWFLSELQWLKRRRAVNPSSRGIFEEMKYLELMIVNDHKTKYKRRSHAHNNF 325
Db 180 KPTTRDMA-LOFTQOTKKRPRM--KREDLSMKYVELIVADYLEQKKRRQODATKIK 236
OY 326 AKSVNIVDSIYKQOLMTRVYLVAVEETWTERKQDIDITNPNOMLHEFSKYRORI--KQHA 383
Db 237 LIETANYDKFYR-SLNIIRIALVGLVWTHGNMCEVSENPYSTLWSFLSWRRKLLAOKYH 295
OY 384 DAVHLISRYTFPHYKRSLSYFGVCS--RTRGVVNEGYELPMVAVOYLSOSLAONLGIOW 441
Db 296 DNAQLITGMSPHGTTIGLAPLMAVCVYOSGVNMDHSENAIGVATMTAHEMGNHGMTH 355
OY 442 EPSSRRKPKDCTESWGCIM-EETGVSHSRKFSKSILEYRDLORGACLEFNR--TK 498
Db 356 DSAD--CCSASADGGCIMAATGHPFKVFNCGNRRLDRLYLOSOGGMCLSNMPDTRM 412
OY 499 LEFTEECNGYVAGEECDCGFHVECYGLCC--KKCSLSNGAHGSDGPCNNNTSCLFQPR 556
Db 413 LVGGRGNGYLEDGEEDCCGEECCNPNCCNASNCTLRPGAECAGHSCCH--QCKLLAP 470
OY 557 GYECDAVNECDITEYCTGDSGCCPPLHKODGYACNONGRCYAGECKTRNOCQYIWG 616
Db 471 GTLCREQARQCDLPECTGKSPHCPTNFYOMDGTCEGQAYCYNMCLITYOEQOQOLMG 530
OY 617 TRAAISDRFCYKLTBEGTEKNGCKD-GDRWIOGSKHDVFCGLTCTNLTRAPRIGOLQ 675
Db 531 PGARPAIDICEKVNAGDITFGNCGKDMNGEHRKCMRDAKCGKIQOCSSEAR--LE 586
OY 676 GEIIP--TSFYHOGVYIDCSGAHVYL----DDOTDVGVEDGTFCGSPSMCLDRKCLQI 728
Db 587 SNAVIDITTIMNGROIQRGTHYRGPEEGDMLPELVMTGKXGNHICFEQOCNRT 646
OY 729 QALNMSCPDLSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKGP 788
Db 647 SFEETEGC-----GKCKNGHGVCCNNONCHCLPGMAPFCNTPGHGSII-----DSGPMPP 697
OY 789 SATNLIIGSINGAILVAIVL 809
Db 698 ESVGPVAVGVLVAILVAILM 718

RESULT 7
US-09-955-504-16
Sequence 16, Application US/09955504
Publication No. US20020182702A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE REFERENCE: PTO06P2
CURRENT APPLICATION NUMBER: US/09/955,504
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,222
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 09/712,907
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: PCT/US00/14308
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/178,717
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/142,930
PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 60/136,388
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 778
TYPE: PRT
ORGANISM: Homo sapiens
US-09-955-504-16

Query Match 22.1% Score 1007.5 DB 9 Length 778:
Best Local Similarity 31.5% Pred. No. 3.1e-60:
Matches 252: Conservative 111: Mismatches 325: Indels 113: Gaps 29:

38 PARTPCRLVLLPPLAASSPRAMGAAPSAPHMNETAEKNGLVLDEDNLTQNS 97
1 PGGAGAAALCLLAFALQPL---RPR-----AAREPCWTRGSEEG----- 37
98 SSNISTSNAMOKETLPSRLIYINODESPYHVLDTKARHQQKHNKAVHLAQSFOIEA 157
1 SPKLOHELLIPQW-----KTSESPV-----REKHPKLKELRYMA 71
38 FGSKEILLDLINGLSSDVEIHY-ENGKPOYS--KGGEHCYHGSIRGKDSKVALST 214
1 EGRELLIDLEKNEQLFAPSYETHTSSGNPQTTTRKLEDFHGTVEBELSSVLTST 131
72 CNGLHGMEF-DTFYVMIPELVLVHDEKSTGRPHIIOKTLAGOYSKOMK---NLTMERG 269
1 CNGLHGMEF-DTFYVMIPELVLVHDEKSTGRPHIIOKTLAGOYSKOMK---NLTMERG 269
132 CRGIGLITVSSNLVIEPLP---DSKG---QHLYR-----SEHLKPPGNGCFEHS 179
270 D-----QMPFLELQMLKRRRAVNPSSRGIFEEEMKYLELMIVNDKTKYKRRSHAHNNF 325
1 KPTTRDMA-LOFTQOTKKRRPRM--KREDLNSMKYVELYVADYLEFOKNRRDQATKHK 236
180 KPTTRDMA-LOFTQOTKKRRPRM--KREDLNSMKYVELYVADYLEFOKNRRDQATKHK 236
326 AKSVNVLVDSITYKEQLNTRVVLAVETWTEKQDIDITTPVOMLHEFSKYRORI--KQHA 383
1 LIEIANYVDKFR-SLNIRIALVGLVHTGNMCEVSENPYSTLMSLRKLLAOKYH 295
237 LIEIANYVDKFR-SLNIRIALVGLVHTGNMCEVSENPYSTLMSLRKLLAOKYH 295
384 DAVHLISRVTFHYKRSLSYFGVCS--RTRGVGVNEYGLPMAVAOYLSQSLAQNLTQW 441
1 DAVHLISRVTFHYKRSLSYFGVCS--RTRGVGVNEYGLPMAVAOYLSQSLAQNLTQW 441
296 DNAQLITGMSFHGTTIGLAPLMAMCSYVQSGGVNMDHSENAIGVATMAHEMCHNFGMTI 355
442 EPSSRRPKCDCTESWGCGIM-EETGVSHSRKFSKCSILEYRDLQRRGGACLPNRP--TK 498
1 EPSSRRPKCDCTESWGCGIM-EETGVSHSRKFSKCSILEYRDLQRRGGACLPNRP--TK 498
356 DSAD---CCSASADGGCIMAATGHPFPKVFNGCNRRELDRLYQSGGMCLSNMPDTRM 412
499 LPEPTGCGNGYVAGEECDCGCFHVECYGLCC--KKCSLSNGAHNSDPCPCNNTSCLPQR 556
413 LYGGRGCGNYLEDGEEDCGEEDCCNPPCCNASNCTLRPGAECARHSCCH--QCKLLAP 470
557 GYECRDVAVNECDITEYCTGDSGOCPPNLIHKODYACNONOGRCYNGECKTRDNOCQYIWG 616
471 GTLCREGARQCDLPREFCTGKSPHCPTNFYQMDGTPCEGGQAYCYNMCILTYOEOCCQQLWG 530
617 TKAAGSDKFCYKELNTEGTEKNGCKD-GDRNIQCSKHDVFCGFLCTLNLTAPRIGTQLO 675
531 PGARPARDLCEFEKVVAVAGDTFGNCGKDMNGEHRKCNMRDAKCGKIQOOSSEARP---LE 586
676 GEIIP--TSFYHOGVAVIDCSGAHYVL-----DDDTVGVYEDGTPPCSPMMLCDRKLQI 728
587 SNAVPIIDTTIIMNGROIQCRGTHYVRGPEEEDMDLPGIYMTGTCYGHNICEEGGCFRNT 646
729 QALNMSSCPILDSKGVCSGHGVCSENEATYICIDFTWAGTDCSIRDPVRNLHPKDEGPKRP 788
647 SEFTEGCG-----GAKCNGHGVCSNNNONCHCLPGRNAPPCNTPRHGGS1-----DSGPRVPR 697
789 SATNIIISIGAILIYAIVL 809
698 ESVGPRVAVGIVAILIYLAIVLM 718

Sequence 4, Application US/10020733
Patent No. US20020161214A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilgenowski, Nathaniel L.
TITLE OF INVENTION: No. US20020161214A1 Human Proteases and Polynucleotides Enco
FILE REFERENCE: LEX-0263-USA
CURRENT APPLICATION NUMBER: US/10/020,733
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: US 60/244,939
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 918
TYPE: PRT
ORGANISM: homo sapiens
US-10-020-733-4

Query Match 22.1% Score 1007.5 DB 9 Length 918:
Best Local Similarity 31.5% Pred. No. 3.9e-60:
Matches 252: Conservative 111: Mismatches 325: Indels 113: Gaps 29:

38 PARTPCRLVLLPPLAASSPRAMGAAPSAPHMNETAEKNGLVLDEDNLTQNS 97
1 PGGAGAAALCLLAFALQPL---RPR-----AAREPCWTRGSEEG----- 37
98 SSNISTSNAMOKETLPSRLIYINODESPYHVLDTKARHQQKHNKAVHLAQSFOIEA 157
1 SPKLOHELLIPQW-----KTSESPV-----REKHPKLKELRYMA 71
38 FGSKEILLDLINGLSSDVEIHY-ENGKPOYS--KGGEHCYHGSIRGKDSKVALST 214
1 EGRELLIDLEKNEQLFAPSYETHTSSGNPQTTTRKLEDFHGTVEBELSSVLTST 131
72 CNGLHGMEF-DTFYVMIPELVLVHDEKSTGRPHIIOKTLAGOYSKOMK---NLTMERG 269
1 CNGLHGMEF-DTFYVMIPELVLVHDEKSTGRPHIIOKTLAGOYSKOMK---NLTMERG 269
132 CRGIGLITVSSNLVIEPLP---DSKG---QHLYR-----SEHLKPPGNGCFEHS 179
270 D-----QMPFLELQMLKRRRAVNPSSRGIFEEEMKYLELMIVNDKTKYKRRSHAHNNF 325
1 KPTTRDMA-LOFTQOTKKRRPRM--KREDLNSMKYVELYVADYLEFOKNRRDQATKHK 236
180 KPTTRDMA-LOFTQOTKKRRPRM--KREDLNSMKYVELYVADYLEFOKNRRDQATKHK 236
326 AKSVNVLVDSITYKEQLNTRVVLAVETWTEKQDIDITTPVOMLHEFSKYRORI--KQHA 383
1 LIEIANYVDKFR-SLNIRIALVGLVHTGNMCEVSENPYSTLMSLRKLLAOKYH 295
237 LIEIANYVDKFR-SLNIRIALVGLVHTGNMCEVSENPYSTLMSLRKLLAOKYH 295
384 DAVHLISRVTFHYKRSLSYFGVCS--RTRGVGVNEYGLPMAVAOYLSQSLAQNLTQW 441
1 DAVHLISRVTFHYKRSLSYFGVCS--RTRGVGVNEYGLPMAVAOYLSQSLAQNLTQW 441
296 DNAQLITGMSFHGTTIGLAPLMAMCSYVQSGGVNMDHSENAIGVATMAHEMCHNFGMTI 355
442 EPSSRRPKCDCTESWGCGIM-EETGVSHSRKFSKCSILEYRDLQRRGGACLPNRP--TK 498
1 EPSSRRPKCDCTESWGCGIM-EETGVSHSRKFSKCSILEYRDLQRRGGACLPNRP--TK 498
356 DSAD---CCSASADGGCIMAATGHPFPKVFNGCNRRELDRLYQSGGMCLSNMPDTRM 412
499 LPEPTGCGNGYVAGEECDCGCFHVECYGLCC--KKCSLSNGAHNSDPCPCNNTSCLPQR 556
413 LYGGRGCGNYLEDGEEDCGEEDCCNPPCCNASNCTLRPGAECARHSCCH--QCKLLAP 470
557 GYECRDVAVNECDITEYCTGDSGOCPPNLIHKODYACNONOGRCYNGECKTRDNOCQYIWG 616
471 GTLCREGARQCDLPREFCTGKSPHCPTNFYQMDGTPCEGGQAYCYNMCILTYOEOCCQQLWG 530
617 TKAAGSDKFCYKELNTEGTEKNGCKD-GDRNIQCSKHDVFCGFLCTLNLTAPRIGTQLO 675
531 PGARPARDLCEFEKVVAVAGDTFGNCGKDMNGEHRKCNMRDAKCGKIQOOSSEARP---LE 586
676 GEIIP--TSFYHOGVAVIDCSGAHYVL-----DDDTVGVYEDGTPPCSPMMLCDRKLQI 728
587 SNAVPIIDTTIIMNGROIQCRGTHYVRGPEEEDMDLPGIYMTGTCYGHNICEEGGCFRNT 646
729 QALNMSSCPILDSKGVCSGHGVCSENEATYICIDFTWAGTDCSIRDPVRNLHPKDEGPKRP 788

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Db 647 SFFTEGCG-----GKCKNGHGVCCNNNONCHCLPQMAAPFCNTPHGSGSI-----DSGEMPP 697
OY 789 SATNLIIGSIGAILVAIVL 809
Db 698 ESVGPPVAGVLAIVLVAIVL 718

RESULT 9
US-10-125-470-9
; Sequence 9, Application US/10125470
; Patent No. US20020165377A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT006P1
; CURRENT APPLICATION NUMBER: US/10/125,470
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/712,907A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/136,388
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/142,930
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/178,717
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-470-9

Query Match 22.1%; Score 1007.5; DB 9; Length 918;
Best Local Similarity 31.5%; Pred. No. 3.9e-60;
Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

OY 38 PARPPCRLVLLPLPLASSRPRANGAAPSAPHNNETREKILNGLADEDNLTLOONS 97
Db 2 PGAGAAALCLLAFALQPL-----RPR-----AAREPGWTRGSEEG----- 37
OY 98 SSNISVSNAOKETILPSRLIYIYNODESPYHVLDTKAHQOKHNKAVHLAQAFOIEA 157
Db 38 -----SPKLOHELIIPQW-----KTSSEPV-----REKHPLKAEILRVMA 71
OY 158 FGSKFILDLLNGLSSDYVEIHY-ENGKPOYS--KGGEHCYHGSIRGVKDSKVALST 214
Db 72 EGRELIDLEKNEQLFAPSYTEHTYSSGNPQTTRKLEDHCFYHGTVRETELSSVTLST 131
OY 215 CNGLHGME-DDTFYVMIETLELVHDEKSTGRPHIIOKTLAOGYSKOMK-----NLTMERG 269
Db 132 CRGIGLTLVSSNSLSYIEPLP---DSKG---OHLIYR-----SEHLRPPGNCGEFHS 179
OY 270 D-----QMPFLSELQWLKRRRAVNPSCGIFEEMKYLELIVNDHKTYKKRRSSHAHTNPF 325
Db 180 KPTTDMMA-LOFTQOTKKRRRM--KREDLNMKIVELVLADYLEFOKNRRDQATKHX 226
OY 326 AKSVNVLVDISYKEQNLTRVLAIVETWTEKQOIDITTPVOMLHEFSKYRQRI--KQHA 383
Db 227 LLEIANVYDKFYR-SLIRIALVGLVEMTHGNMCEVSENPSTLMSFLSMRRRLAKQKH 295
OY 384 DAVHLISRTVEHYKRRSSLSYFGVCS--RTRGVGVVEYGLPMVAQVLSLSLAQNQIGIOW 441
Db 226 DNAQLTGTSPFTTITGLAPLMAKMSVYSGGVNMDHSENALGVAATMAHEMHNFGMTH 355
OY 442 EPPSRKPKDCETESWGGCJIM-EETGVSHSRKSKCSILEYRDFLQRGGAQLFNRP--TK 498
Db 356 DSAD---CCSASADGCGCIMAATGHPKPVFNGCRRELDRYLQSGGWCJLSNMPDTRM 412
OY 499 LREPEECNGYVAGCECCGCFVEVEYGLCC--KKCSLSGAMCSGPGCCNNTSCLEFQR 556
Db 413 LVGGRGCGNGYLEDEGECDCGEEBECNPNPCNNSCTLRPGACAGSGCH--QCKLLAP 470
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OY 557 GYECRDVAVNECDITTEYCTGDSGCPENLHKODGYACANONQRCYNGECKTRDNOCQYIWG 616
Db 471 GTLCREARQCDLLEPFCYKSPHCFPTNLYOMDGTPEBGGAIVCYNGMGLTYQEOCQOLMG 530
OY 617 TKAAGSDKCYEKLNTGTEGKNGCKD-GDRWIOCSKHDFVFCGLCTNLTRAPRIGLO 675
Db 531 PGARPAPDLCEKVVAVDGTFCNGCKDMNGEHRKCMMDAKCGKITQCCSSSEARP-----LE 586
OY 676 GEIIP--TSFYHOGAVIDCSGAHYVL-----DDDTFVGVEDEGTPCGSPMCLDRKQLOI 728
Db 587 SNAVPIDTITLIMGHQIQCRGTHVYRGPPEBESDMLPGLVMTGTGCTGNHICFEQCCANT 646
OY 729 QALNMSCPDLSKGVCSGHGVCSEATCICDFTWAGTDCSIRDPVRNLHPKDEGPRGP 788
Db 647 SFFTEGCG-----GKCKNGHGVCCNNNONCHCLPQMAAPFCNTPHGSGSI-----DSGEMPP 697
OY 789 SATNLIIGSIGAILVAIVL 809
Db 698 ESVGPPVAGVLAIVLVAIVL 718

RESULT 10
US-10-125-452-9
; Sequence 9, Application US/10125452
; Patent No. US20020173640A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT006P2
; CURRENT APPLICATION NUMBER: US/10/125,452
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/955,504
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 09/712,907
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: PCT/US00/14308
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/178,717
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/142,930
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/136,388
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-452-9

Query Match 22.1%; Score 1007.5; DB 9; Length 918;
Best Local Similarity 31.5%; Pred. No. 3.9e-60;
Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

OY 38 PARPPCRLVLLPLPLASSRPRANGAAPSAPHNNETREKILNGLADEDNLTLOONS 97
Db 2 PGAGAAARCLLAFALQPL-----RPR-----AAREPGWTRGSEEG----- 37
OY 98 SSNISVSNAOKETILPSRLIYIYNODESPYHVLDTKAHQOKHNKAVHLAQAFOIEA 157
Db 38 -----SPKLOHELIIPQW-----KTSSEPV-----REKHPLKAEILRVMA 71
OY 158 FGSKFILDLLNGLSSDYVEIHY-ENGKPOYS--KGGEHCYHGSIRGVKDSKVALST 214
Db 72 EGRELIDLEKNEQLFAPSYTEHTYSSGNPQTTRKLEDHCFYHGTVRETELSSVTLST 131
OY 215 CNGLHGME-DDTFYVMIETLELVHDEKSTGRPHIIOKTLAOGYSKOMK-----NLTMERG 269
Db 180 KPTTDMMA-LOFTQOTKKRRRM--KREDLNMKIVELVLADYLEFOKNRRDQATKHX 226
OY 326 AKSVNVLVDISYKEQNLTRVLAIVETWTEKQOIDITTPVOMLHEFSKYRQRI--KQHA 383
Db 227 LLEIANVYDKFYR-SLIRIALVGLVEMTHGNMCEVSENPSTLMSFLSMRRRLAKQKH 295
OY 384 DAVHLISRTVEHYKRRSSLSYFGVCS--RTRGVGVVEYGLPMVAQVLSLSLAQNQIGIOW 441
Db 226 DNAQLTGTSPFTTITGLAPLMAKMSVYSGGVNMDHSENALGVAATMAHEMHNFGMTH 355
OY 442 EPPSRKPKDCETESWGGCJIM-EETGVSHSRKSKCSILEYRDFLQRGGAQLFNRP--TK 498
Db 356 DSAD---CCSASADGCGCIMAATGHPKPVFNGCRRELDRYLQSGGWCJLSNMPDTRM 412
OY 499 LREPEECNGYVAGCECCGCFVEVEYGLCC--KKCSLSGAMCSGPGCCNNTSCLEFQR 556
Db 413 LVGGRGCGNGYLEDEGECDCGEEBECNPNPCNNSCTLRPGACAGSGCH--QCKLLAP 470
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180 KPTTRDMA-LOFTQOTKKRRPRM--KREDLNSMKYVELYLAVADYLEFOKNRRDODATYHK 236
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237 LIEIANYVDKPYR-SLIRIALVGLVETWTHGNMCEVSENYPSTLWSPFLSMRRKLAAQYH 295
384 DAVHLISRYTFHYKRRSLSYFGVCS--RTRGVNVETGLPMAVAQVLSOSLAQNLGIOW 441
296 DNQOLITGMSPHGTITGLAPLMAVCYQSGVNMDSHSENAIGVATMAHEMGNHFGMTH 355
442 EPSSRRKPKCDTESWGCIM-EETGVSHSRKFSKCSILEYRDLORGGACLEFNR--TK 498
356 DSAD--CCSASAADGSCIMAAATGHPFKYFNGCNRELDRLYLQSGGCMCLSNMPTRM 412
499 LPEPTGCGVNEAGECDGCFHVECYGLCC--KCSLSNGAHCSGDCGCGNNTSCLEFPR 556
413 LYGRRCGNGYLEDGECDGEEBECNNPCSNASCTLRPGAECAGHSCCH--QCKLLAP 470
557 GYECRDVNECDITEYCTGDSGOCPPNLHKODGYACNONOGRVNGECKTRDNOCOYIWG 616
471 GTLCREQARQCDLPEFCTGKSPHCPTNFYQMDGTPCEGGAUYCYNGMCLTYOEQCOQLMG 530
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531 PGARPADLCEFEKYNVAGDTFGNCGKDMNGEHRKCMNRDAKCGKIOCCSSEARP---LE 586
676 GEIIP--TSFYHOGVRIDSGAHVVL-----DDTDVGYVEDTGPCGSPMCLDRKLOI 728
587 SNAVPIDTITIMNGROIQCRGTHYVRGPEEGMDLPGLVMTGTCGYNHICFEGOCRT 546
729 QALNMSSCPIDSKGVCSGHVCSENEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKP 788
647 SFETEGC-----GKCNNGHGVCCNNONCHCLPGMAPRPFCTMPGHGGSI-----DSGMP 697
789 SATNLIIGSIAGAILVAIVL 809
698 ESVGPAVAGVLAIVLAVLM 718

RESULT 11

US-09-955-504-9
; Sequence 9, Application US/09955504
; Publication No. US20020182702A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO06P2
; CURRENT APPLICATION NUMBER: US/09/955, 504
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234, 222
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 09/712, 907
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: PCT/US00/14308
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/178, 717
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/142, 930
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/136, 388
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-955-504-9

Query Match 22.1%, Score 1007.5; DB 9; Length 918;
Best Local Similarity 31.5%, Pred. No. 3.9e-60;
Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

38 PARTPCRLLLVLLPLPLAASSPRAMGAAPASAPMNETAKNLGLADEDNLTQONS 97
2 PGAGAACRLCLAFALNPL-----RPR-----AAREGWTGRSSEG----- 37
98 SSNISYSNAMQKEITPLSRILYIYNODESPRYHVLDTKARHQQKHNKAHVAQASFOIEA 157
38 -----SPKLQHELLIPQW-----KTSSEPV-----REKHLKAEILVMA 71
158 FCSKFLIDLILNGLLSSIVYEIHY-ENGRPOVS--KGEHCYHGSIRKVRKSKVALST 214
72 EGRELLIDLEKNEQLEFAPSYLETTHYSSGNPQTTKRLLEDHCYHGTVRETELSSVTLS 131
215 CGLHOMFE-DTPFYMIPLLELVHDEKSTGRPHIIOKTLAOGYSKOMK-----NLTMERG 269
132 CGIGRLITVSSNLVIERLP---DSKG---OHLYR-----SEILKRPNGCEPHS 179
180 KPTTRDMA-LOFTQOTKKRRPRM--KREDLNSMKYVELYLAVADYLEFOKNRRDODATYHK 236
326 AKSVNLVDSIYKCOLNTRVVLAVETWTEKDOIITTNPVQMLHEFSKYRORI--KQHA 383
237 LIEIANYVDKPYR-SLIRIALVGLVETWTHGNMCEVSENYPSTLWSPFLSMRRKLAAQYH 295
384 DAVHLISRYTFHYKRRSLSYFGVCS--RTRGVNVETGLPMAVAQVLSOSLAQNLGIOW 441
296 DNQOLITGMSPHGTITGLAPLMAVCYQSGVNMDSHSENAIGVATMAHEMGNHFGMTH 355
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356 DSAD--CCSASAADGSCIMAAATGHPFKYFNGCNRELDRLYLQSGGCMCLSNMPTRM 412
499 LPEPTGCGVNEAGECDGCFHVECYGLCC--KCSLSNGAHCSGDCGCGNNTSCLEFPR 556
413 LYGRRCGNGYLEDGECDGEEBECNNPCSNASCTLRPGAECAGHSCCH--QCKLLAP 470
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531 PGARPADLCEFEKYNVAGDTFGNCGKDMNGEHRKCMNRDAKCGKIOCCSSEARP---LE 586
676 GEIIP--TSFYHOGVRIDSGAHVVL-----DDTDVGYVEDTGPCGSPMCLDRKLOI 728
587 SNAVPIDTITIMNGROIQCRGTHYVRGPEEGMDLPGLVMTGTCGYNHICFEGOCRT 546
729 QALNMSSCPIDSKGVCSGHVCSENEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKP 788
647 SFETEGC-----GKCNNGHGVCCNNONCHCLPGMAPRPFCTMPGHGGSI-----DSGMP 697
789 SATNLIIGSIAGAILVAIVL 809
698 ESVGPAVAGVLAIVLAVLM 718

RESULT 12

US-10-020-733-2
; Sequence 2, Application US/10020733
; Patent No. US20020161214A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgenowski, Nathaniel L.
; APPLICANT: Fiddie, Carl Johan
; TITLE OF INVENTION: NO. US20020161214A1 Human Proteases and Polynucleotides Enco
; FILE REFERENCE: LEX-0263-USA
; CURRENT APPLICATION NUMBER: US/10/020, 733
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244, 939
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2
LENGTH: 926
TYPE: PRT
ORGANISM: homo sapiens
US-10-020-733-2

Query Match 22.18; Score 1007.5; DB 9; Length 926;
Best Local Similarity 31.5%; Pred. No. 3,9e-60;
Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

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QY 38 PARTPPCRLLVLLPLPLAASSRPRMAAAPSAPPHNETAEKNLGLADEDNLTQONS 97
Db 2 PGAGAGARLCLLAFALOPL----RPR-----AAREPGWTRGSEEG----- 37
QY 98 SSNISYSNMAOKETLPSRLIYYINDSESPYHLDTRKHQOKHNKAVHLAQSFOIEA 157
Db 38 -----SPKQHELIIFQW-----KTESPV-----REKHPLKAEILRYMA 71
QY 158 FGSKFIIDLINNGILSSDVEIHY-ENGKPOYS--KGEGHYHGSIRGVKDSKVALST 214
Db 72 EGRELLIDLKRNQLEFAPSTETHYTSSGNQDTTRKLEDCFYHGTVRETELSSVTLST 131
QY 215 CNGLHGME-DPTFVYIEPLELVHDEKSTGRPHIIQTLAQSOKM---NLTMERG 269
Db 132 CRGIRGLITSSNLSYIEPLP---DSKG---QHLYR-----SEHLKPPNGGFEHS 179
QY 270 D---QMPLESEIOWLKRRAVNPSPGIEEMKYLELMIVNDHKTYKKHRSNAHTNNE 325
Db 180 KPTTRDMA-LQFTQOTKKRRRM--KREDLSMKYVELYLADYLEFQKNRRDQDATKHK 236
QY 326 AKSVVNVDSIYKQOLNTRVYLAVETWTEKDQIDITNPVQMLHEFSKYRORI--KQHA 383
Db 237 LIETANVVDKPYR-SLIRIALVGLVWTHGNMCEVSENPYSTLSFSLMRKLLAOKYH 295
QY 384 DAVHLISRVTFFHYKRSSLSYFGVCS--RTRGVNEXGLPMAVAOYLSLSIAQNLGIOW 441
Db 296 DNMOLITGMSFHGTIGLAPLMAACSVYQSGVNMHDSENAIGVAATMAHEMGHFGMTH 355
QY 442 EPPSRKPKCDCTESWGGCIM-EETGVSHSRKFSKCSILEYRDFLORGGAQLFNRP--TK 498
Db 356 DSAD---CCSASADGGCIMAATAAGHPKPVKFNCGNRRDLRYLOSGGMCLSNMPDTRM 412
QY 499 LFEPTGCGNGYVEAGEEDCGFHEVCYGLCC--KKCSLSNGAHGSDGPCNNTSCLFQPR 556
Db 413 LYGGRRCNGNYLEDEGEEDCGEEECNPNPCNASNCTLRPGAECAGHSGCH--QCKLLAP 470
QY 557 GYECRDVNECDITEYCTGDSGQCPRLHKQDGYACNONGRCYNGECKTRDNOCQYIWG 616
Db 471 GTLCREQARQCDLPEFCTGKSPHCPTNFYOMDGTPECEGQAVCYNGMCLTYOEOCQOLWG 530
QY 617 TKAGSDKFCYEKINTEBTEKNGCKGD-CDRWIQSKHDVFCGFLCNTLTPARIGOLQ 675
Db 531 PGARPADLCEKFNAGVADTGFNGCKGDMNGEHRKCMRDACGKIQCOSSSEARP---LE 586
QY 676 GEIIP--TSFYHGRVIDSGAHVVL-----DDDTVGVEEDGTPCGSPMCLDRKCLQI 728
Db 587 SNAVPIDITTIMNGRIQCRGTHYRGPEEGSDMLDPGLVMGTGCKGYNHICFEGQCRNT 646
QY 729 QALNNSSCPILDSKGVCSGHCVCSEATCICDFTWAGTDCSTRDPVRLHPKDEGPKCP 788
Db 647 SFFETEGC-----GKKCNHGVCNNNQNCHCLPGWAPFCNTPGHGSGI---DSGPMPP 697
QY 789 SATNLIIGISAGALIVAAIVL 809
Db 698 ESVGPPVAGVAILVLAIVLM 718
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Search completed: June 1, 2003, 18:54:49
Job time : 129 secs

7 4547 99.9 6391 61 US-60-172-360-21719 Sequence 21719, A
8 4540 99.7 6401 65 US-60-213-359-127 Sequence 127, App
9 4186 91.9 4440 30 US-09-760-484-15 Sequence 15, App
10 3917.5 88.0 2271 80 US-60-360-207-15737 Sequence 15737, A
11 3851 86.6 4720 24 US-09-631-534-9 Sequence 9, App
12 3851 84.6 4720 43 US-10-260-506-9 Sequence 9, App
13 3621 79.5 2268 24 US-09-631-534-1 Sequence 1, App
14 3621 79.5 2268 31 US-09-809-617-1 Sequence 1, App
15 3621 79.5 2268 31 US-09-809-790-1 Sequence 1, App
16 3621 79.5 2268 43 US-10-260-506-1 Sequence 1, App
17 3202 70.3 2127 24 US-09-631-534-11 Sequence 11, App
18 3202 70.3 2127 43 US-10-260-506-11 Sequence 11, App
19 3007 66.0 2088 24 US-09-631-534-3 Sequence 3, App
20 3007 66.0 2088 31 US-09-809-617-3 Sequence 3, App
21 3007 66.0 2088 31 US-09-809-790-3 Sequence 3, App
22 3007 66.0 2088 43 US-10-260-506-3 Sequence 3, App
23 2687 59.0 2959 18 US-09-496-321-82 Sequence 82, App
24 2687 59.0 2959 18 US-09-496-321-109 Sequence 109, App
25 2687 59.0 2959 55 US-60-118-905-82 Sequence 82, App
26 2687 59.0 2959 55 US-60-118-905-109 Sequence 109, App
27 2295 50.4 1340 65 US-60-212-656-550 Sequence 550, App
28 2295 50.4 1340 65 US-60-212-656-550 Sequence 550, App
29 2003 44.0 3231 80 US-60-360-207-3346 Sequence 3346, App
30 1992.5 43.8 4063 23 US-60-278-232-1862 Sequence 1862, App
31 1992.5 43.8 4063 23 US-09-607-200-6443 Sequence 6443, App
32 1985 43.6 2604 24 US-09-634-252a-5 Sequence 5, App
33 1985 43.6 2604 42 US-10-202-675-5 Sequence 5, App
34 1983 43.6 4400 76 US-60-324-185-31780 Sequence 31780, App
35 1983 43.6 4400 76 US-60-213-359-2451 Sequence 2451, App
36 1960 43.0 2359 65 US-60-212-656-767 Sequence 767, App
37 1958 43.0 2578 65 US-60-212-656-745 Sequence 745, App
38 1947.5 42.8 4411 61 US-60-172-360-26703 Sequence 26703, App
39 1750.5 38.4 3402 42 US-09-760-484-177 Sequence 177, App
40 1750.5 38.4 3402 42 US-10-211-364-395 Sequence 395, App
41 1750.5 38.4 3402 42 US-10-216-893-114 Sequence 114, App
42 1750.5 38.4 3402 42 US-10-217-651-164 Sequence 164, App
43 1680 36.9 1668 80 US-60-360-207-18137 Sequence 18137, App
44 1680 36.9 1668 80 US-09-792-2008-17 Sequence 17, App
45 1680 36.9 1668 30 US-09-792-200C-17 Sequence 17, App

ALIGNMENTS

RESULT 1
US-09-634-252a-2
Sequence 2, Application US/09634252A
GENERAL INFORMATION:
APPLICANT: Ceretti, Douglas P.
TITLE OF INVENTION: SVPB3-13 AND SVPB3-17 DNA AND POLYPEPTIDES
FILE REFERENCE: 03260 0051-00304
CURRENT APPLICATION NUMBER: US/09/634,252A
CURRENT FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 60/074,310
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 2499
TYPE: DNA
ORGANISM: Homo sapiens
US-09-634-252a-2
Alignment Scores:
Pred. No.: 3,44e-302 Length: 2499
Score: 4553.00 Matches: 832
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
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1 ATGAAGCCGCGCGGAGCAGCTCGCGGAGCGCCCGCTCGCGGCTGCAGCTTCGCGGCG 60
21 ATASerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
61 GCTTCTCTGCGGCGCCGACGCGGCGCGCGCGCTGCGGCTGCGGCGCGCGCGCGCG 120
41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer 60
121 ACGCGCGCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
61 ArgProArgAlaArgGlyAlaAlaProSerAlaProHisTrpAsnGluTrpAlaGlu 80
181 CG 240
81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100
241 AAAAATTGGAGATCTGCGAGATGAAGAATACATTCACAGCAAGATGACGACCTAAT 300
101 LLeSerTrpSerAsnAlaMetGlnLysGluLeuThrLeuProSerArgLeuLeuLeu 120
301 ATCAGTTACAGCAATGCAATGCAAGAAAGAAATCAGCTGCTTCAAGCTCATATTTAC 360
121 LLeAsnGlnAspSerGlySerProGlyHisValLeuAspThrLysAlaArgHisGln 140
361 ATCAACCAAGACCTGCGAAGCCCTTATACGCTTCTTACACCAAGCAAGCAAGCAAG 420
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421 AAACATATATAGGCTGTCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
161 LysPheLeuLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTrpValGluIle 180
481 AAATTCATCTTCTGACCTCATGCAATGCAATGCTTGTGCTTGTGCTTGTGCTTGT 540
181 HisTrpGlnAsnGlyLysProGlnTrpSerCysGlyLysGluHisCysTrpTrpHisGly 200
541 CACTACGAAATATGGCAACCACTACTACTAGGCTGAGAGCACTGTTACTACATGAGA 600
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601 AGCATACAGCGCGGCAAGACCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
221 MetPheGlnAspAspThrPheValTrpMetIleGluProLeuGluLeuValHisAspGlu 240
661 ATGTTTGAAGATGATATCTGCTGATATGATGATGATGATGATGATGATGATGATG 720
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781 ATGAAGAAATCTCATATGAAAGAGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTG 840
281 LeuLysArgArgGlyArgAlaValAsnProSerArgGlyIlePheGluGluMetLysTrp 300
841 TTGAAGAAAGAGAAAG 900
301 LeuGluLeuMetIleValAsnAspHisLysTrpTrpLysLysHisArgSerSerHisAla 320
901 TTGGAACCTTATATCTTCTTATATGATCATCAAAAGCTTAAGAACATGCGCTTCATG 960
321 HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTrpLysGln 340
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QY      561 ArgAspAlaValAsnGlyCysAspIleThrGlyTyrCysThrGlyAspSerGlyGlyCys 580
Db      1681 CGGGATGGCTGACAGAGTGCATATTACTGAATATTGTAAGTGCATCTGCTCACTGC 1740
QY      581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlyArgCysTyr 600
Db      1741 CCACCAAAATCTTCATACAGCAAGACGATGATGCATCAAAATCAGGCGCGCTGATC 1800
QY      601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleTrpGlyThrLysAlaAla 620
Db      1801 AATGGCGAGTGCAAACACGAGACCAACGAGTGCATCATCTGGGGAGAACAAAGCGCTGCA 1860
QY      621 GlySerAspLysPheCysTyrGlyLysLysLeuAsnThrGluGlyThrGlyLysGlyAsnCys 640
Db      1861 GGGCTGACAACTTCTGCTATGAAAGCTGATACGAAGGCGCATAGAAAGGAAACTGC 1920
QY      641 GlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660
Db      1921 GGGAGAGATGGAGACCGGTGATTCAGTGCACAAACATGATGATGTTCTGTGATTCCTTA 1980
QY      661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyIleIleIlePro 680
Db      1981 CTTCTACCAAACTTACTGAGCTCCACGTAATTTGGCACTTCAGGTGAGATCAATCCCA 2040
QY      681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValAlaLeuAsp 700
Db      2041 ACTTCCTTCTACCAATCAAGCGCGGTGATTCAGTGCAGTGCATGATGATTTTATGAT 2100
QY      701 AspAspThrAspValGlyTyrValGlyAspGlyThrProCysGlyProSerMetMetCys 720
Db      2101 GATGTATACGATGTGGGTATGTAGAAAGATGGAACCCCATGTGGCCGCTATGATATGTGT 2160
QY      721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740
Db      2161 TTAGATCGGAAGTGCCTACAAATTCAGGCCCTTAATATATGACAGGTGTCTCAGTGAATCC 2220

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QY      741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGlnAlaThrCysIleCysAsp 760
Db      2221 AAGGTTAAAGTCTTTTGGGCGCATGGGTTGTGTAGTATAGAACACCTGCATTTGTAT 2280
QY      761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780
Db      2281 TTCACCTGGCGACAGAGACAGATTCAGTATCCGGATCCAGTTAGGAACCTTCACCCCCC 2340
QY      781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
Db      2341 AAGGATGAAGACCCCAAGGGCTGATGTCACCAATTCATAAATAGCGTCCATCGTGGT 2400
QY      801 AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTrpGlyPheLysAsnValLys 820
Db      2401 GCCATCTCGTACGACCTATTGTCTTGCGGGGACAGCGTGGGATTTAAATATGTCAAG 2460
QY      821 LysArgArgPheAspProThrGlnGlnGlyProIle 832
Db      2461 AAGAGAGGTTCGATCCTACTCAGCAAGGCCCATC 2496

RESULT 2
US-10-202-675-2
: Sequence 2, Application US/10202675
: GENERAL INFORMATION:
: APPLICANT: Cerrecti, Douglas P.
: TITLE OF INVENTION: SVP#3-13 AND SVP#3-17 DNA AND POLYPEPTIDES
: FILE REFERENCE: 03260, 0051-00304
: CURRENT APPLICATION NUMBER: US/10/202,675
: CURRENT FILING DATE: 2002-07-23
: PRIOR APPLICATION NUMBER: US/09/634,252
: PRIOR FILING DATE: 2000-08-07
: PRIOR APPLICATION NUMBER: 60/074,310
: PRIOR FILING DATE: 1998-02-11
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 2
: LENGTH: 2499
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-202-675-2

Alignment Scores:
Pred. No.: 3,44e-302 Length: 2499
Score: 4553.00 Matches: 832
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 42

US-09-634-252A-4 (1-832) x US-10-202-675-2 (1-2499)
QY      1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20
Db      1 ATGAAGCGCGCGCGCACAGCTCGCGACGCGCGCGCGCTGCGAGCTTGCCTGCGCGC 60
QY      21 AlSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
Db      61 GCTTCTGCGCGCGCGCACAGCGCGCGCGCGCTGCGGCTGCGAGCGCGCGCGCGC 120
QY      41 ThrProCysArgLeuLeuValLeuLeuLeuLeuLeuProProLeuAlaAlaSerSer 60
Db      121 ACGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY      61 ArgProArgAlaTrpGlyAlaAlaAlaAlaProSerAlaProHisTrpAsnGluThrAlaGly 80
Db      181 CGGCGCGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGC 240
QY      81 LysAsnLeuGlyValLeuAlaAspGlyAspAsnThrLeuGlnGlnAsnSerSerSerAsn 100
Db      241 AAAAATTTGGGAGTCTGCGCAGATGAAGACATATCATTTGCACAGATAGCAGCAGTAT 300
QY      101 IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrTyr 120

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Db ATCAGTTACACCAATGCATGCAAGAAATCAACATGCCCTTCAAGACTATATATAC 360
OY ILeasnInaspSerGluSerProThyrHisValIleuAspThrLysAlaArgHisGln 140
OY 121 ILeasnInaspSerGluSerProThyrHisValIleuAspThrLysAlaArgHisGln 140
Db 361 ATCAACCAAGACTCGGAAAGCCCTTATCACGTTCTTGACACAAAGCAAGACACAGCA 420
OY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160
Db 421 AAACATATTAAGGCTGCTCATCTGGCCACAGCAACCTTCCAGANTGAAGCCCTTCGCTCC 480
OY 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspThrAlaGluIle 180
Db 481 AAATTCATCTTGACCTCATCTGAACAATGGTTGTTGTTCTTGATTAATGTCAGATT 540
OY 181 HisTyrGluAsnGlyLysProGlnTyrSerLysGlyGluHisCysTyrTyrHisGly 200
Db 541 CACTACGAAATGGGAAACCAACAGTACTCTAAGGGTGGAGACACTGTTACTACACATGGA 600
OY 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220
Db 601 AGCATCAGAGGCGCTCAAGACTCCAAAGGTGCTCTGTCAACTGCATGCAATGACTTTCATGCG 660
OY 221 MetPheGluAspAspThrPheValTyrMetIleGluProLeuGluLeuValHisAspGlu 240
Db 661 ATGTTGAAGATGATACCTTCGTGATATGATAGAGCCACTAGAGCTGCTTCATGATGAG 720
OY 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260
Db 721 AAACACACAGCTGCACCAATATATCCAGAAACCTTGGCAGACAGATTCATGACAA 780
OY 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerGluLeuGlnTyr 280
Db 781 ATGAAGAATCTCATATGAGAAAGAGGTGACAGTGGCCCTTCTCTCAATTAACAGTGG 840
OY 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGluGluMetLysTyr 300
Db 841 TTGAAAAGAGAGAGAGAGAGAGTGAATCCATCAGCTGATATATTGAAGAAATGAATAT 900
OY 301 LeuGluLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAla 320
Db 901 TTGGAACCTTATGATGTTATGATCATCAAAACGTATAAAGACATGCGCTTCCTCATGCA 960
OY 321 HisThrAsnAsnPheAlaLysSerValLysAsnLeuValAspSerIleTyrLysGluGln 340
Db 961 CATACCAACACTTGTCCAAAGTCCGTGTCACCTTGTGATTCCTATTACAGAGAGCAG 1020
OY 341 LeuAsnThrArgValValLeuValAlaValGluThrTyrPheGluLysAspGlnIleAsp 360
Db 1021 CTCACACACAGGGTGTCTCGTGGCTGTAGAGACCTGGACGTGAAGATCAGATTGAC 1080
OY 361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIleLys 380
Db 1081 ATCACCACCAACCTTGTGAGATGCTCATGAGCTTCAAAATACCGGCGCCCATTAAG 1140
OY 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysAspSerSer 400
Db 1141 CAGCAGCTGATGCTGTGACCTCATCTCGGGGTGATTCATTCATTAAGAGAGACAGT 1200
OY 401 LeuSerTyrPheGlyLysValCysSerArgThrArgGlyValGlyAlaAsnGluTyrGly 420
Db 1201 CTCGAGTTACTTGGAGGTGTCTGTCTCCGCAAGAGAGAGTGTGGTGTGATGATGATG 1260
OY 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440
Db 1261 CTTCACATGCGACATGCGACAAAGTATATCCAGAGCTGCTCAAAACCTTGGATCAA 1320
OY 441 TrpGluProSerSerArgLysProLysCysAspCysThrGlnSerTyrGlyLysIle 460
Db 1321 TGGGAACCTTCTGACGAGAAAGCCAAATGTGATGCGACAAATCTTGGGTGGCTGATC 1380
OY 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr 480
|||||

Db 1381 ATGAGAGAAACAGGGGTGTCCCATTTCTGCAAAATTTTCAAAATGCGACATTTGGAGTAT 1440
OY 481 ArgAspPheLeuGlnArgGlyLysAlaCysLeuPheAsnArgProThrLysLeuPhe 500
Db 1441 AGAGACTTTTTCACAGAGAGAGAGAGTGGAGCTCCCTTTCACAGAGCCAAACCAAGCTATTT 1500
OY 501 GluProThrGluCysGlyLysAsnGlyTyrValIleGluAlaGlyGluCysAspCysGlyPhe 520
Db 1501 GAGCCACGAGATGTGGAAATGATACGTGGAAGCTGGGAGAGAGTGTGATGTTGGTTT 1560
OY 521 HisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540
Db 1561 CATGTGAATGCTATGAGATTAATGCTGTAGAAATGTTCCCTCCCAACGGGCTCACTGC 1620
OY 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgLysTyrGlyCys 560
Db 1621 AGCGAGGGCCCTGCGTGAACATACCTCATGCTTTTTCAGCCACAGAGGTATGATGC 1680
OY 561 ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCys 580
Db 1681 CGGATGCTGTGACAGAGTGTATATTACTGAATATTGTACTGAGACTGTGTCAGTGC 1740
OY 581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyr 600
Db 1741 CCACCAATCTTCATTAAGCAAGACGATATGATGCAATCAAAATCAGGCGCTGCTAC 1800
OY 601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleThrPheLysHisAlaIle 620
Db 1801 AATGGCGAGTGCAGACCAAGACCAACAGTGCATCATCATCTGGGGAACAAAGGCTGCA 1860
OY 621 GlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGluLysGlyAsnCys 640
Db 1861 GGTGTGACAGTGTCTGATGAAAGCTGAATACAGAAAGCACTGAGAAAGGAAACTGC 1920
OY 641 GlyLysAspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660
Db 1921 GGGAGAGATGCAAGACCGGTGATTCAGTCAGCAAAACATGATGTTGTTCTGTGATTTCA 1980
OY 661 LeuCysThrAsnLeuThrArgAlaProArgIleGluGlnLeuGlnGlyIleIlePro 680
Db 1981 CTCTGTACCATCTTACTGAGCTCCACGTATTTGCTCACTTGAAGGTGAGATCATTTCCA 2040
OY 681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValValLeuAsp 700
Db 2041 ACTTCCCTTACCATCAAGCCGCGGTGATTGACTGACGTGCGCTCATGATGTTAGAT 2100
OY 701 AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720
Db 2101 GATGATACGGATGTGGCTATGTAGAAGATGAAGCCCATGTGGCCGTATGATGTGT 2160
OY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740
Db 2161 TTGAGTGGAGAGTGTCTCAAAATTCAGCCCTAAATGTAGAGAGCTGCCAGCTGATTCC 2220
OY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760
Db 2221 AAGGTTAAAGTGTGTGGGCGAATGGGCTGTAGTAAAGCAACCTGCATTTGTGAT 2280
OY 761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValAlaArgAsnLeuHisProPro 780
Db 2281 TTCACTGGGCGAGGACAGATTCAGATATCCGGATCCAGTTAGGAACCTTACACCCCCC 2340
OY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
Db 2341 AAGGATTAAGGACCAAGGAGGCTAGTGCCACCAATCTCAATTAAGGCTCATGCTGCTG 2400
OY 801 AlaIleLeuValAlaAlaIleValIleValLeuGlyLysThrGlyTyrGlyPheLysAsnValLys 820
Db 2401 GCCATTCCTGTAAGCAGCATATGCTTGGGGGACAGGCTGGGATTTAAAAATGTCAG 2460
OY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832
Db 2461 AAGAGAAGGTTGTGATCTACTACAGAGGCCCATC 2496
|||||

Db	2637	AGGAGAGGGCCGCTGTACAAATACCTCAATGCTTTTTCAGCCACGAGGATATGAAATGC	2696
Qy	561	ATGAspAlaValAsnGluCysAspIleThgIuTyrCysThrGlyAspSerGlyGlnCys	580
Db	2697	CGGATGCTCTGTGAACGAGTGTGATATTTCGAATATTGTACTGGAGACTCTGGTCAGTGC	2756
Qy	581	ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyAlaTyrCysTyr	600
Db	2757	CCACCAATTTCTCATTAAGCAAGACGATATGCATGCATCAATCAAAATTCAGGGCGCTGCAC	2816
Qy	601	AsnGlyGluCysLysThrIleArgAspAsnGlnCysGlnTyrIleTrrpGlyThhLysAlaAla	620
Db	2817	AATGGCGACAGTCGAAGACAGACAGACACACAGTCACTGATCAATCTGGGGAACAAAGCTGCA	2876
Qy	621	GlySerAspLysPheCysTyrGluLysLeuAsnThrGlnGlyThrGluLysGlyAsnCys	640
Db	2877	GGGTCTACAAAGTTCTGCTATGAAAGCTGCAATTCAGAAAGCACTGAGAAAGGAAATGCG	2936
Qy	641	GlyLysAspGlyAspArgTrrpIleGlnCysSerLysHisAspValPheCysGlyPheLeu	660
Db	2937	GGGAAGATGAGAGACCGGTGGATTCAGTCAGCAACACATGATGTGTCTGTGGATTTCTTA	2996
Qy	661	LeuGlyHisAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlnGlyIleTrrp	680
Db	2997	CTGTGACCAATCTTACTCGAGCTCCACGTAATGTGCTCACTTCAGGGTGAATCTTTCCA	3056
Qy	681	ThiSerPheTyrHisGlnGlyAlaArgValIleAspCysSerGlyAlaHisValAlaLeuAsp	700
Db	3057	ACTTCCTCTTCCATCAACAGCCGGGTGATTCAGTCACTGAGGCCCATGTATGTTTAAGAT	3116
Qy	701	AspAspHisAspValGlyTyrValGlnAspGlyThrProCysGlyProSerMetMetCys	720
Db	3117	GATATATCGGAGTGGGCTATGTAGAAAGATGGAACGCCATGTGGCCCGCTATATGATGTGT	3176
Qy	721	LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer	740
Db	3177	TTAATATCGAAGTGCCTCAATTCACAGCCCAATATAGACAGCTGTGCACATTCATGCC	3236
Qy	741	LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp	760
Db	3237	AAGGTAAAGCTGTTCGGCCATGGGGCTGTGTACTAATGAAGCCACCTGACTTTGTGAT	3296
Qy	761	PheThrTrrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisIlePro	780
Db	3297	TTTACCTTGGCAGGACGACATTCGACATTCGGGATTCAGTATGAGAACCTTCACCCCCC	3356
Qy	781	LysAspGlnGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly	800
Db	3357	AAGGATGAAGACCCACAGGCTCTAGTGCACCAATCTCATATATAGGCTCCATCCGTGCT	3416
Qy	801	AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTrrpGlyPheLysAsnValLys	820
Db	3417	GCCATCCCGTAGACGACTATTTGCTTTGGGGGCACAGGCTGGGGATTTAAAAATGTCAAG	3476
Qy	821	LysArgArgPheAspProThrGlnGlnGlyProIle	832
Db	3477	AAGAGAGGTTGATCTACTCAGACAGGCCCCATC	3512
RESULT 4			
US-09-976-594-61			
: Sequence 61, Application US/09976594			
: GENERAL INFORMATION:			
: APPLICANT: Furness, Michael			
: TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS			
: FILE REFERENCE: PA-0041 US			
: CURRENT APPLICATION NUMBER: US/09/976,594			
: CURRENT FILING DATE: 2001-10-12			
: PRIOR APPLICATION NUMBER: 60/240,409			
: PRIOR FILING DATE: 2000-10-12			
: NUMBER OF SEQ ID NOS: 1143			
: SOFTWARE: PERL Program			
: SEQ ID NO 61			

	:	LENGTH: 6400	
	:	TYPE: DNA	
	:	ORGANISM: Homo sapiens	
	:	FEATURE:	
	:	NAME/KEY: misc_feature	
	:	OTHER INFORMATION: Incyte ID No: 037502.4	
	:	US-09-976-594-61	
		Alignment Scores:	
		Pred. No.: 1,09e-301	Length: 6400
		Score: 4553.00	Matches: 832
		Percent Similarity: 100.00%	Conservative: 0
		Best Local Similarity: 100.00%	Mismatches: 0
		Query Match: 100.00%	Indels: 0
		DB: 36	Gaps: 0
		US-09-634-2524-4 (1-832) x US-09-976-594-61 (1-6400)	
QY		1 MetLysPProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly	20
Db		224 ATGAAAGCGCGCGGAGAGCTCGCGGACGCCGCCCTGGCGGGCTCAGCCCTTGGCGGC	283
QY		21 AlaSerCgGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg	40
Db		284 GCTTCTCTGGGGCCCCCAAGCGGGCGCGCGCTCGGGGCTGCGACGCCCGCGCGCGC	343
QY		41 ThrProProCysArgLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer	60
Db		344 ACGCGCGCCCTCGCGCTGCTTCTGCTCTCTGCTGCTCGCTCGCTCGCGCGCTCGTC	403
QY		61 ArgProAlaGlyATrPGlyAlaAlaAlaProSerAlaProHisTrpAsnGlnThrAlaGlu	80
Db		404 CGGCGCGCGCGCTGGGGGGCTGCTGCGCGCGCGCTCGCATTTGGATTGAACATCGAGAA	463
QY		81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn	100
Db		464 AAAATTGTGGAGCTCTGCGAGATGAAACAAATACATTGCAACGAAATAGCAGCAGTAAT	523
QY		101 ILeserTyrrSerAspAlaMetGlnLysGlnLuehrLeuProSerArgLeuIleTyrTrp	120
Db		524 ATCACTTACAGCAAAATGCAATGAGAAAGAAATACACACTGCTTACAGACTATATATTAC	583
QY		121 ILesnGlnAspSerGlnSerProTrpHisValLeuAspThrLysAlaArgHisGlnGln	140
Db		584 ATCAACCAAGACTCGGAAAGCCCTTATCAGCTTGTGACACAAAGCAGACACACAA	643
QY		141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGlnAlaPheGlySer	160
Db		644 AAACATTAATTAAGCGTGCATCTGCGCCAGGCAACCTTCAGATTGAAGCCCTTGCGCTC	703
QY		161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGlnIle	180
Db		704 AAATTTCATTCTTGACCTCATCTGTAACAATGGTTTGTTGCTCTTGATTATGTGGAGATT	763
QY		181 HisTyrGluAsnGlyLysProGlnTyrSerLysGlyGlyGlnHisCysTyrTyrHisGly	200
Db		764 CACTACGAAAGGGGAAACACACAGTACTTAAGGGTGAAGACATGTTACTATACATGA	823
QY		201 SerIleArgGlyValLysAspSerLysValAlaIleAspSerThrCysAsnGlyLeuHisGly	220
Db		824 ACACATCAGAGCGGCTGAACAACTCCAGAGGCGCTCTGTCAACCTGCAATGAGACTTCATG	883
QY		221 MetPheGluAspAspThrPheValTyrMetIleGluProLeuGlnLeuValHisAspGlu	240
Db		884 ATGTTTGAAGATGATACCTTCTGTATATGATAGAGCCACTGAGACTGTTATCATGATGAG	943
QY		241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln	260
Db		944 AAAAGCAGCGGTGACACATTAATTCACAGAAACCTTGGCGAGCAGAGATTCTTAAGCAA	1003
QY		261 MetLysAsnLeuThrMetGluArgGlyAspGlnTrpProPheLeuSerGlyLeuGlnTrp	280
Db		1004 ATGAAAGATCTCAGTATGGAAGAGGTGACGATGGCCCTTTCTCTGGAATTACATGG	1064

QY 281 LeuLysArgArgLysArgAlaValAsnProSerArgLysIlePheGluGluMetLysTyr 300
|||||
Db 1064 TTGAAAGAGAGAGAGAGAGAGAGATCATCATGATGATATATTGAAAGAAATGATAT 1123
QY 301 LeuGluMetLysIleValAsnAspHisLysThrTyrLysLysHisArgSerHisAla 320
|||||
Db 1124 TTGGAACTTTATGATTTGATTAAGATCACAAACGATTAAGAACGATCGCTTCATCA 1183
QY 321 HisThrAsnAspPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGluGln 340
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Db 1184 CATACCAACAACCTTGCAGAGTCCGTGTCACCTTGATGATTTCTATTACAGAGAGCAG 1243
QY 341 LeuAsnThrArgValValLeuValAlaValGluThrTrpThrGluLysAspGlnIleAsp 360
|||||
Db 1244 CTCACACACAGAGGTGTCCTGCTGGCTGTAGAGACCTGAGACGAGAGATCAGATTGAC 1303
QY 361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIleLys 380
|||||
Db 1304 ATCACCAACAACCTTGCAGATGCTCCATGAGTTCTCAAAATACCGGACGAGCTTGAAG 1363
QY 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSer 400
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Db 1364 CAGCATCTGATGCTGTGACACCTCATCTCCGGGTGACATTTCACTATAGAGAGAGAGT 1423
QY 401 LeuSerTyrPheGluGluValLysSerArgThrArgLysAlaGluValAsnGluTyrGly 420
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Db 1424 CTGAGTACTTTGGAGGTGCTGTTCTCGCACAGAGAGAGTTGCTGATAGAGTAAGT 1483
QY 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGluIleGln 440
|||||
Db 1484 CTTCCAATGGCAGAGGACCAAGATATATCCGACAGCCGCTCAAAACCTTGGAATTCGA 1543
QY 441 TrpGluProSerSerArgLysProLysCysAspCysThrGlnSerTrpGluGlyCysIle 460
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Db 1544 TTGGAACTTTCTACAGCAAAACCAAAATGTACTGACAGAGATCTGGGGTGGCTGATC 1603
QY 461 MetGluIleThrGluValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr 480
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Db 1604 ATGGAGGAAACAGGGGTGTCCTCATTCGAAATTTTCAAAATGTCAGCATTTTGAATAT 1663
QY 481 ArgAspPheLeuGlnArgGlyGlyAlaLysLeuPheAsnArgProThrLysLeuPhe 500
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Db 1664 AGAGACTTTTACAGAGAGAGGAGGAGCCCTTTTCAACAGGCCCAACAACTATTTT 1723
QY 501 GlnProThrGluCysGlyAsnGlyTyrValGluAlaGluGluGluCysAspCysGlyPhe 520
|||||
Db 1724 GAGCCCAAGGAGATGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1783
QY 521 HisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540
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Db 1784 CATGTGGAATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1843
QY 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGluCys 560
|||||
Db 1844 AGCAGCGGCGCTCTTAACAAATACCTCATGCTTTTTCAGCCAGGAGGATGATGATGAT 1903
QY 561 ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyCys 580
|||||
Db 1904 CGGGATCTGTGAACGAGTGTGATATTAATATTTGATGAGACTCTGGGTAGTGC 1963
QY 581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyr 600
|||||
Db 1964 CCACCAATATCTTCAAGCAAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 2023
QY 601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleTrpGlyThrLysAlaVal 620
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Db 2024 AATGGCAGGTGCAAGACCAAGACAGATGATGATGATGATGATGATGATGATGATGATGAT 2083
QY 621 GlySerAspLysPheCysTyrGluLysLeuAsnThrGluGluIleGlyLysGlyCys 640
|||||
Db 2084 GGGTCTGACAAAGTTCTGCTATGAACCTGAAATACAGAGGCACCTGAGAGAGGAACCTGC 2143

QY 641 GlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660
|||||
Db 2144 GCGAAGGATGAGAGACCGGTGATTCAGTGCAGCAAAACATGATGTTCTGTGATGATCTTA 2203
QY 661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyIleIlePro 680
|||||
Db 2204 CTCTGTACCAAACTTACTGACGCTCCACGTAATGCTCAACTTCAGGCTGAGATCATTCGA 2263
QY 681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValIleValAsp 700
|||||
Db 2264 ACTTCTTCTACCATCAAGCCCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 2323
QY 701 AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720
|||||
Db 2324 GATGATACGAGATGTGGCTGTATGAGAAGATGGAACGCAATGTGGCCCTGATGATGATGAT 2383
QY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740
|||||
Db 2384 TTAGATCGGAAAGCCCTTACAAATTCAGCCCTAAATATGAGACAGCTTCACATCGATTC 2443
QY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760
|||||
Db 2444 AAGGTAAGATCTGTTCTGGGCTCATGGGTGTGATGATGATGATGATGATGATGATGATGAT 2503
QY 761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780
|||||
Db 2504 TTACACTGGGACAGAGACAGATTCAGATTCGGGATCATTTAGGAACCTTCACCTTCATGAT 2563
QY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
|||||
Db 2564 AAGGATGAAGAGACCAAGGCTCTAGTCCACCAATCTCAATATAGCTCCATCCGCTGCT 2623
QY 801 AlaIleLeuValAlaIleValIleValLeuGlyGlyTyrGlyTrpGlyPheLysAsnValLys 820
|||||
Db 2624 GCCATCTGCTGACAGCTATGTTCTTGGGGCAGACAGCTGGGATTTAAATGATCAAG 2683
QY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832
|||||
Db 2684 AAGAGAAAGTTGATCTACTACAGCAAGGCCCATC 2719

RESULT 5

US-60-240-409-61
; Sequence 61, Application US/60240409
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STIM
; FILE REFERENCE: PA-0041 P
; CURRENT APPLICATION NUMBER: US/60/240,409
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 61
; LENGTH: 6400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 037502.4
US-60-240-409-61

Alignment Scores:

Pred. No.:	1,09e-301	Length:	6400
Score:	4553.00	Matches:	832
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	68	Gaps:	0

US-09-634-252a-4 (1-832) x US-60-240-409-61 (1-6400)

QY 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20
|||||

Db 224 ATGAAGCCGGCCGAGCAGCTCGGGGACGCCGCCCTGCGGGCTGACCTTGCCGCC 283
Qy 21 AlaSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
Db 284 GCTTCCTCGGGCCCGCAACGGGGCCCGCGCTCGGTGCTGCCAGCGCCCGCCGCCG 343
Qy 41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer 60
Db 344 ACGGGCCCTCGCCCTGCT 403
Qy 61 ArgProAlaGlyAlaTyrGlyAlaAlaAlaProSerSerAlaProHisTyrPaspGluThrAlaGlu 80
Db 404 CGGGCCCGGGCTGGGGGGCTGCTGCCGCCGCCCTCCGCTTGGAAATGAACATGCGAGAA 463
Qy 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerSerAsn 100
Db 464 AAAAATTTGGAGCTCGTGGCAGATGAAGACAAATCATTCGCAACAGATAGACAGATAT 523
Qy 101 IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrTyr 120
Db 524 ATCAGTTACAGCATGCAATGCAAGAAAGAAATACACTGCTTCAGACATCATATATATAC 583
Qy 121 IleAsnGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaAlaGHisGlnGln 140
Db 584 ATCAACCAAGACTCGAAGACCCCTTATCAGCTTCTTGACACAAAGCAAGCAACACGCA 643
Qy 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGlnAlaPheGlySer 160
Db 644 AAACATATATAGGCTGTCATCTGCGCCAGGACGCTTCAGATGTGAAGCCTTGCGCTCC 703
Qy 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIle 180
Db 704 AAATTCATCTTCACTCATCTGACATGAAACATGTTGTTGTTCTCTGATATATGAGAT 763
Qy 181 HisTyrGluAsnGlyLysProGlnTyrSerLysGlyGlyLysGlyLysGlyTyrHisGly 200
Db 764 CACTACAAATATGGAAACCAACGACTACTTAAGGGTGGAGACGACTTAACTACATGCA 823
Qy 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220
Db 824 AGCATAGAGGCTCAAAAGACTCCAAAGTGGCTCTGTCACACTGCAATGAGACTTCATG 883
Qy 221 MetPheGluAspAspThrPheValIleTyrMetIleGluProLeuGluLeuValHisAspGlu 240
Db 884 ATGTTTGAGATGATACCTTCTGCTGATATGATAGACCACTAGAGGTGCTTCAATGATG 943
Qy 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260
Db 944 AAAGACAGAGTGCACACATATATCCAGAAACCTTGCGACAGACAGATATTCAGCA 1003
Qy 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerLysLeuGlnTyr 280
Db 1004 ATGAAATCTCTCTATGGAAGAGGTGACCAAGTGGCCCTTCTCTCTAAATTCAGTGG 1063
Qy 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGluGlnMetLysTyr 300
Db 1064 TTGAAAGAAGAGAGAGACAGATCCATCCACGCTGATATTTCAAAATGAAATAT 1123
Qy 301 LeuGluLeuMetIleValAsnAspHisLysTyrTyrLysLysHisArgSerSerHisAla 320
Db 1124 TTGGACTTATGATGTTGATATATATACAAACGTATAAAGAACATCCGCTCTCTCATG 1183
Qy 321 HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGluGln 340
Db 1184 CATACCAACACTTTGCAAAAGTCCGTGCACACTTGCGATTTCTATTTACAGAGACAG 1243
Qy 341 LeuAsnThrArgValValLeuValAlaValGluThrTyrPheGluLysAspGlnIleAsp 360
Db 1244 CTCACACACAGGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1303
Qy 361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgGlyLys 380
Db 1304 ATCACCACCAACCCGTGTGAGATGCTCCATGAGTTCTCAAAATACCGGACGCAATTAAG 1363

Qy 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSer 400
Db 1364 CAGCATGCTGATCTGTGACACCTCATCTCGGGGTGACATTTCTCATATGAAGAACAG 1423
Qy 401 LeuSerTyrPheGlyGlyValLysSerArgThrArgGlyValGlyValAsnGlyLysGly 420
Db 1424 CTGAGTTACTTTTGAGAGTGTCTCTCTCTCGCACAGAGAGTTGGTGTGATGATGATG 1483
Qy 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440
Db 1484 CTTCATATGCGACTGCGACAGATATATGCAAGAGCCTGGCTCAAAACCTTGAAATCCA 1543
Qy 441 TrpGluProSerSerArgLysProLysCysAspCysThrGluSerTyrGlyLysGly 460
Db 1544 TGGGAACCTTTTACGCAAGAAAGCCAAATGATGATGACAGAAATCTGGGGGTGCTCAT 1603
Qy 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr 480
Db 1604 ATGAGAGAAACAGGGGTGTCCCATTCGCAAAATTTTCAAAAGTCAGCATTTTGAGAT 1663
Qy 481 ArgAspPheLeuGlnArgGlyGlyGlyAlaCysLeuPheAsnArgProThrLysLeuPhe 500
Db 1664 AGAGACTTTTATACAGAGAGAGGTGAGCTGCTCTTTCACAGGCCCAAAACCTATTT 1723
Qy 501 GluProThrGluCysGlyAsnGlyTyrValGluAlaGlyGlyGlyCysAspCysGlyPhe 520
Db 1724 GAGCCACGGAATGTGGAATGATACGTGGAAGCTGGGAGAGATGTGATTTGCTTTT 1783
Qy 521 HisValGluCysTyrGlyLeuGlyCysGlyLysGlySerLeuSerAsnGlyAlaHisCys 540
Db 1784 CATGTGAGATGCTATGAGATATGCTGTAGAAATGTCTCTCTTCCAAAGGGCTTCAAC 1843
Qy 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGlyCys 560
Db 1844 ACGAGCGGGCCCTGCTGATACATACCTCATGCTTTTTCAGCCAGAGGATATGAATG 1903
Qy 561 ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyLys 580
Db 1904 CGGATGCTGTAGAGAGGTGATATATCTGAATTTTACTGAGACTGTGCTGACAGTGC 1963
Qy 581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnIleArgCysTyr 600
Db 1964 CCACCAAAATCTTCATAGACAGACGATATGATGATGCAATCAAAATCAGAGCGCTGC 2023
Qy 601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleTyrPheGlyThrLysAla 620
Db 2024 AATGGCGAGTGCAGACAGACAGACAGACAGTGTGATCATCTGCGGAAACAAAGCTG 2083
Qy 621 GlySerAspLysPheCysTyrGlyLysLeuAsnThrGluGlyThrGluLysGlyAsnCys 640
Db 2084 GGGTCTGACAAAGTTGCTGTATGAAGAGCTGAATACAGAGCACTGCAAGAGGAAATGC 2143
Qy 641 GlyLysAspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660
Db 2144 GGAAGAGTGAAGACCGGTGATTCAGTGCAGCAAACTGATGTCTGTGCGATTTCTTA 2203
Qy 661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyIleIlePro 680
Db 2204 CTCTGTACCAATCTTACGCGAGCTCCAGCTATGCTGATCACTTCAGGGTGAATATTTCA 2263
Qy 681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValLeuAsp 700
Db 2264 ACTTCCTCTCATCATCAAGCGCGGTGTGACGAGTGTGCTCCATGTAGTTTATGAT 2323
Qy 701 AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720
Db 2324 GATGATACGATGTGGGTATGTATGAAATGAAAGCCCATGTGGCCCGCTCATCATGTGT 2383
Qy 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740
Db 2384 TTAGATGCGGAAGTGCCTAACAAATTCAGCCCTTAATATGAGCAGCTGTCCACATCGATTC 2443

OY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760
|||||
Db 2444 AAGGTTAAAGTCTGTTCGGGCGCATGGGTGTAGTAATGAAGCCACCTGATTTGTGAT 2503
OY 761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780
|||||
Db 2504 TTCACCTGGGAGGAGGAGATTGACGTATCCGGGATCCAGTTAGGAACCTTCACCCGCC 2563
OY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
|||||
Db 2564 AAGATGTAAGAGCCCAAGAGCTCTAGTGCACCAATCTATATAGGCTCCATCGCTGGT 2623
OY 801 AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTrpGlyPheLysAsnValLys 820
|||||
Db 2624 GCCATCCGTGTAGACAGTATGCTCTGGGGGACACAGCGCTGGGATTTAAATGTCAAG 2683
OY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832
|||||
Db 2684 AAGAGAAAGTTCGATCTACTCAGCAAGGCCCATC 2719

RESULT 6

US-60-324-185-1573

Sequence 1573, Application US/60324185

GENERAL INFORMATION:

APPLICANT: Morris, MacDonald

APPLICANT: Lal, Preeti

APPLICANT: Diep, Dinh

TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING

TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY

TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY

FILE REFERENCE: GX-0019-1 P

CURRENT APPLICATION NUMBER: US/60/324,185

NUMBER OF SEQ ID NOS: 35862

SOFTWARE: PERL Program

SEQ ID NO 1573

LENGTH: 6400

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc. feature

OTHER INFORMATION: Incyte ID No: 037502.4

US-60-324-185-1573

Alignment Scores:

Pred. No.:	1-09e-301	Length:	6400
Score:	4553.00	Matches:	832
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-634-252a-4 (1-832) x US-60-324-185-1573 (1-6400)

OY 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20
|||||
Db 224 ATGAAGCGCGCGGAGCAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 283
OY 21 AlaSerGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
|||||
Db 264 GCTTCTCGGCG 343
OY 41 ThrProCysArgLeuLeuLeuValLeuLeuLeuProProLeuAlaAlaSerSer 60
|||||
Db 344 ACG 403
OY 61 ArgProAlaGlyTrpGlyAlaAlaAlaProSerAlaProHisTrpAsnGluThrAlaGlu 80
|||||
Db 404 CGGCG 463
OY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100
|||||
Db 464 AAAAATTTGGGAGTCTGGCAGATGAAGCAATATACATTGCAACAGATAGACAGCTAAT 523

OY 101 IleSerTrpSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTrpTrp 120
|||||
Db 524 ATCAGTTACAGCAATGCAATGCAAGAAATCACTACCTGCTTCAAGCTATATATTAC 583
OY 121 IleAsnGlnAspSerGluSerProTrpHisValLeuAspThrLysAlaArgHisGln 140
|||||
Db 584 ATCAACCAAGACATCGGAACCCCTTATCAGCTTCTTACACAAAGCAAGCACACAGCA 643
OY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160
|||||
Db 644 AACATATATAGGCTGTCATCTGGCCAGGCAAGCTTCAGATTGAAGCCCTGGCCGCC 703
OY 161 LysPheIleLeuAsnLysLeuLeuAsnGlyLeuLeuSerSerAspTrpValGluIle 180
|||||
Db 704 AAATTCATTTCTTGACCTCATCTAGCAAAATGCTTTGTTGCTTCTTCTGATTAATGAGATT 763
OY 181 HisTrpGluAsnGlyLysProGlnTrpSerLysGlyGluHisCysTrpTrpHisGly 200
|||||
Db 764 CACTACGAAATGGAACACACAGTACTTAAAGGTGAGAGCACTGTTACTACCATGCA 823
OY 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerTrpCysAsnGlyLeuHisGly 220
|||||
Db 824 AGCATCAGAGGCGTCAAGACTCCAGAGTGGCTGTCAACTCCAAATGAGACTTCATGCG 883
OY 221 MetPheGluAspAspThrPheValTrpMetIleGluProLeuGluLeuValHisAspGlu 240
|||||
Db 884 ATGTTTAACATGATGATCTCTGCTGTATATGATATAGGACACAGTACAGCTGATGATAG 943
OY 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTrpSerLysGln 260
|||||
Db 944 AAAAGCACAGCTGCACCAATATATATCCAGAAACCTTGGCAGAGCAAGTATTTCAAGCAA 1003
OY 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTrpProPheLeuSerGluLeuGlnTrp 280
|||||
Db 1004 ATGAGATCTCAGTATGGAAGAGGTGACAGTGGCTTCTCTCTGAAATTTACAGTGG 1063
OY 281 LeuLysArgArgLysArgAlaValAlaAsnProSerArgGlyIlePheGluGluMetLysTrp 300
|||||
Db 1064 TTGCAAAAGAAAGAAAGAGAGAGAGTGAATCCATCAGCTGATATTGGAAGAAATGAATAT 1123
OY 301 LeuGluLeuMetIleValAsnAspHisLysThrTrpLysLysHisArgSerSerHisAla 320
|||||
Db 1124 TTGGAACTTATGATTTGTAATGATCACAAACGTAATAAGAGCATCGCTTCTCATGCA 1183
OY 321 HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTrpLysGlnGln 340
|||||
Db 1184 CATACCAACAACCTTGGCAAGTCCGTGCTCAACCTTGTGATTTTACAAAGCAGCAG 1243
OY 341 LeuAsnThrArgValValLeuValAlaValGlnTrpTrpTrpGluLysAspGlnIleAsp 360
|||||
Db 1244 CTCACACACAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
OY 361 IleThrTrpAsnProValGlnMetLeuHisGluPheSerLysTrpArgGlnArgLys 380
|||||
Db 1304 ATCAACCAACAACCTTGGCAAGTCCGTGCTCAACCTTGTGATTTTACAAAGCAGCAG 1363
OY 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTrpLysArgSerSer 400
|||||
Db 1364 CAGATCTCTATGCTGTGACCTCATCTCGGGGTGACATTTCATTAAGAAGAACGCT 1423
OY 401 LeuSerTrpPheGlyGlyValCysSerArgTrpArgGlyValGlyValAsnGluTrpGly 420
|||||
Db 1424 CTGAGTTACTTTGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
OY 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440
|||||
Db 1484 CTTCCAATGTCAGTGGCAACAAGTATATCCGAGAGCCTGAGTCAAAACCTTGGATCAAA 1543
OY 441 TrpGluProSerSerArgLysProLysCysAspCysTrpHisGlySerTrpGlyCysIle 460
|||||
Db 1544 TGGGAACCTTCTAGCAAGAAAGCCAAATGTGACAGATCTGGGTGGCTGCATTC 1603

QY 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr 480
DB 1604 ATGGAGAAACAGGGGTCCTCCATTCGAAATTTTCAAGATGTCACGATTTGGAGTAT 1663
QY 481 ArgAspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsnArgProThrLysLeuPhe 500
DB 1664 AGAAGCTTTTTCAGAGAGAGGGTGGAGCCCTTTTCAACAGGCCAACCAACTATTT 1723
QY 501 GluProThrGlyCysGlyAsnGlyTyrValGluAlaGlyGluGlyCysAspCysGlyPhe 520
DB 1724 GAGCCCAACGAAATGGAATAGTACTGGAACTGGGAGGAGTGTGATTTGTTT 1783
QY 521 HisValGlyCysTyrGlyLeuCysCysLysCysSerLeuSerAsnGlyAlaHisCys 540
DB 1784 CATGTGGAATGCTATGTATGTATGCTGTAAGAAATGTTCCCTCTCCACGGGGCTCAGTGC 1843
QY 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGlyCys 560
DB 1844 AGCAGCGGGCCCTGTAACAAATACCTCATGTCTTTTTCAGCCACGAGGGTATGATGC 1903
QY 561 ArgAspAlaValAsnGlyCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCys 580
DB 1904 CGGATGCTGTGACAGATGTGATTTACTGATATTTGCTGAGACTCTGTCAGTGC 1963
QY 581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyr 600
DB 1964 CCACCAAACTTTCATTAACCAAGACGAGATGTCATCAAAATCAGAGCGCGCTGTAC 2023
QY 601 AsnGlyGlyCysLysThrArgAspAsnGlnCysGlnTyrIleTyrGlyThrLysAlaAla 620
DB 2024 AATGGCGAGTGCACAAACAGACAGACACAGAGTGTGATGTCAGTGGGAGACAAAGCTGCA 2083
QY 621 GlySerAspLysPheCysTyrGlyLysLeuAsnThrGlnGlyThrGlnLysGlyAsnCys 640
DB 2084 GGGTGTGACAACTTGTCTATTAAGAGCTGATACAGAACGACAGAGAGGAGAACTGC 2143
QY 641 GlyLysAspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660
DB 2144 GGAAGAGATGAGAGACGGGTGATTCAGTCCAGCAAAATGATGTCTGTGATGATTTTCA 2203
QY 661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyIleIlePro 680
DB 2204 CTCTGACCAATCTTACTGACCTCCAGCTATTTGGTCAACTTCAGAGGTAGATTCCTCA 2263
QY 681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValIleAsp 700
DB 2264 ACTTCCTTACCATCAACAGCGGGGTGATGACTGACAGTGGTCCCATTTAGAT 2323
QY 701 AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720
DB 2324 GATGATACCGATGTGGCTATGTAGAAGATGGAACCCCATGTGGCCGCTATGATGTGT 2383
QY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740
DB 2384 TTAGATCGGAATGCTTACAAATTCAGCCCTTAATATGACAGCTGTCCACCGATTC 2443
QY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760
DB 2444 AAGGGTAAAGTCTGTCGGGCCCATGGGCTGTAGTAATGAAGCCACCTGCAATTTCTGAT 2503
QY 761 PheThrTyrAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780
DB 2504 TTCACCTGGGACAGGAGAGATTCAGATTCGCGGATTCAGATTAAGAACTTCACCCCCC 2563
QY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
DB 2564 AAGGATGAGAGACCCCAAGGCTCTAGTCCACCAATCTCTAATAGCTTCATCCCTGCT 2623
QY 801 AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTyrPheLysAsnValLys 820
DB 2624 GCCATCTCTGTACAGCTATTGTCTGTGGGGCAGACAGGCTGGGATTTAAATAATGTCAAG 2683
QY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832

DB 2684 AAGAGAGGTTGCATCTTACTACGACAGGCCCATC 2719
RESULT 7
US-60-172-360-21719
: Sequence 21719, Application US/60172360
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preclt
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: FILE REFERENCE: GX-0007 P
: CURRENT FILING DATE: 1999-12-16
: NUMBER OF SEQ ID NOS: 29838
: SOFTWARE: PERL Program
: SEQ ID NO 21719
: LENGTH: 6391
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 037502.4
: NAME/KEY: unsure
: LOCATION: 4043-4060, 4177, 4359, 4494
: OTHER INFORMATION: a, t, c, g, or other
US-60-172-360-21719
Alignment Scores:
Pred. No.: 2,86-301 Length: 6391
Score: 4547.00 Matches: 831
Percent Similarity: 99.88% Conservative: 0
Best Local Similarity: 99.88% Mismatches: 1
Query Match: 99.87% Indels: 0
DB: 61 Gaps: 0
US-09-634-252a-4 (1-832) x US-60-172-360-21719 (1-6391)
QY 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20
DB 224 ATGAGCGCGCCCGGAGAGAGCTCGCGGCGAGCGGCCCTTGGGCTGCAAGCTTGGCGC 283
QY 21 AlaSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
DB 284 GCTTCTCGGCGCCCAACAGCGGCGCGCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCT 343
QY 41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuProProLeuAlaAlaSerSer 60
DB 344 AGCGCGCCCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
QY 61 ArgProArgAlaTyrGlyAlaAlaAlaProSerAlaProHisTyrAsnGluThrAlaGlu 80
DB 404 CGGCCCGCGCGCTGGGGGCTGCTGCGCCGCGCGCTGCGCATTTGAATGAATTCACAGA 463
QY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100
DB 464 AAAAATTTGGAGTCTGCGAGATGACATTAATTCATTCGAACCAATTAAGCAGCTAAT 523
QY 101 IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrTyr 120
DB 524 ATCAGTACAGCAATGCAATGCAAGAAATACACACTGCTTCAAGACTCATATATATAC 583
QY 121 IleAsnGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaArgHisGlnGln 140
DB 584 ATCAACCAAGACTCGGAAGCCCTTATCAAGTCTTGACCAAGGAGGAGACACAGCA 643
QY 141 LysHisAsnLysAlaValaHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160
DB 644 AAACATTAATTAAGCTGCTGCTGCTGCGCCAGGCAAGCTTCAGATTAACCTTGGCTCC 703
QY 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIle 180

|||||
Db 704 AATTCATTCCTTGACCTCAGTGAACAAAGTTGTGTCTCTGATTTATGTGGAAATT 763
Oy 181 H1STYRGLUASNGLYLSPROGINTYRSELYSGLYGLUNH1SCSYTYRTH1SGLY 200
Db 764 CACTACGAAATGGGAAACACAGTACTCTAAGGGTGGAGACACTTCTACACATGGA 823
Oy 201 Ser11eArgLYValLysAspSerLYsValAlaLeuSerThrCysAsnGLYLeuH1SGLY 220
Db 824 ACACATCAGAGCGGCTCAAGAGTGGCTCTGTCACACCTGCAATGACATTCATGGC 883
Oy 221 MetPheGLUAspAspThrPheValTYRMet11eGLUProLeuGLUeUValH1SAspGLU 240
Db 884 ATGTTGGAAGATGATACCTTCGTGATATGATGACCCACTAGAGCTGCTTCAATGAGAG 943
Oy 241 LysSerThrGLYArgProH1S11eGLINLysThrLeuValGLYGLN1YRSELYSGLY 260
Db 944 AAAGACAGAGGTGGACACATATATCCAGAAACCTTGGCAGACAGTATTCTACACAA 1003
Oy 261 MetLYsAsnLeuThrMetGLUArgGLYAspGLN1YRProPheLeuSerGLUeUValTYR 280
Db 1004 ATGAAAGAAATCTCAATGGAAGAGGTGACCACTGCGCCCTTCTCTGAAATTAACATGG 1063
Oy 281 LeuLYsArgArgLYsArgAlaValAsnProSerArgGLY11ePheGLUeUValTYR 300
Db 1064 TTGAAAAGAGAGAGAGACAGTGAATCCATCCAGTGTATATTGAAAGAAATGAATAT 1123
Oy 301 LeuGLUeUValMet11eValAsnAspH1S1YRThrLYsLYsH1SAspSerH1S1Ala 320
Db 1124 TTGGAACCTTATGATTTGATATGATCAAAACGTAATAGAGAGATCCCTTCTCAACGA 1183
Oy 321 H1STHrAsnAspPheAlaLYsSerValValAsnLeuValAspSer11eTYRGLYGLN 340
Db 1184 CATACCAACAACTTGGCAAGTCCGTGGTCAACCTTGTGATTTATTAAGAGACAG 1243
Oy 341 LeuAsnThrArgValValLeuValAlaValGLN1YRThrPheGLUeUValAspGLN1Leas 360
Db 1244 CTCACACACAGGGGTGTCTGTGGCTGTAGAGACCTGGACAGAGGATCAGATGAC 1303
Oy 361 11eThrThrAspProValGLN1eUValH1SGLUPheSerLYsTYRArgGLN1YRGLY 380
Db 1304 ATCACCACCAACCCCTGTGCAGATGCTCCATGACTTCTCAAAATACCGGACCCCATTAAG 1363
Oy 381 GLNH1SAlaAspAlaValH1SLeu11eSerArgValThrPheH1STYRLYsArgSer 400
Db 1364 CAGCATGCTGATGCTGTGCACCTCATCTCGCGGTGACATTTCACTAATAGACAGACAGT 1423
Oy 401 LeuSerTYRPhelGLYGLYValCysSerArgThrArgGLYAlaGLYValAsnGLUTYRGLY 420
Db 1424 CTGAGTTACTTTGGAGGTGTCTGTCTCCACAAAGAGAGTTGGTGAATGAGTAAGT 1483
Oy 421 LeuProMetAlaValAlaGLN1ValLeuSerGLN1SerLeuAlaGLN1AsnLeuGLY11eGLN 440
Db 1484 CTTCCAATGGAGTGGCACAAGATATATGCGACAGGCTGGCTCAAAACCTTGGAAATTCAA 1543
Oy 441 TRPG1UProSerSerArgLYsProLYsCysAspCysThrGLN1SerTRPG1YGLYCYH1e 460
Db 1544 TGGGAACCTTCTAGCAGAAAGCCAAATGTGACTGCACAGAAATCCGTGGGTGCTGATC 1603
Oy 461 MetGLUeUValThrGLYValSerH1S1eArgLYsPheSerLYsCysSer11eLeuGLN1TYR 480
Db 1604 ATGGAGGAACAGGGGTGTCCCATTTCTCGAAATTTTCAAGAGCATTTGGAGATAT 1663
Oy 481 ArgAspPheLeuGLN1ArgGLYGLYAlaCysLeuPheAsnArgProThrLYsLeuPhe 500
Db 1664 AGAGACTTTTACAGAGAGAGGTGAGCTGCCCTTTCAACAGGCCCAACAAAGCTATTTT 1723
Oy 501 GLUProThrGLYCysGLYAsnGLYTYRValGLUAlaGLYGLN1UCysAspCysGLYPhel 520
Db 1724 GAGCCCCACGGAATGTGGAATGATGATCGTGAAGAGCTGGGGAGAGAGTGTATGTGGTTT 1783
Oy 521 H1SValGLUCysTYRGLYLeuCysLYsLYsCysSerLeuSerAsnGLYAlaH1SCys 540
|||||

Db 1784 CATGTGAAGTCTATGATTAATGCTGTAAAGAAATGCTCCCTCCACAGGGGCTCACTGC 1843
Oy 541 SerAspGLYProCysCysAsnAsnThrSerCysLeuPheGLN1ProArgGLYTYRGLUCys 560
Db 1844 AGCCAGGGGCGCTGCTGTAAACATTAATCTCATGTCTTTTTCACGCCAGGGGTATGAATGC 1903
Oy 561 ArgAspAlaValAsnGLUCysAsp11eThrGLUTYR1YR1YR1YR1YR1YR1YR1YR1YR 580
Db 1904 CGGATGCTGTGAACAGATGTGATATCTGAAATATTTGTACTGGAGACTGTGCTAGTGC 1963
Oy 581 ProProAsnLeuH1S1YRGLN1AspGLYTYRAlaCysAsnGLN1AsnGLYArgCysTYR 600
Db 1964 CCACCAATCTTCAATTAACCAAGAGATATCATGCAATCAAAATCAGAGCGCGCTGTAC 2023
Oy 601 AsnGLYGLUCysLYsThrArgAspAsnGLN1YRGLN1YR11eTRPG1YRThrLYsAla 620
Db 2024 AATGGCGAGTCCAAAGACCAAGACAGAGTGTGCTCATCTGTGGGAAACAAAGCTGCA 2083
Oy 621 GLYSerAspLYsPheCysTYRGLYLeuAsnThrGLUeUValTYRGLYGLYAsnGLY 640
Db 2084 GGGTCTGACAAATTCCTGCTATGAAAGCTGAATACAGAAAGCACAGAGAGGAAAGCTGC 2143
Oy 641 GLYLYsAspGLYAspArgTRP11eGLN1CysSerLYsH1SAspValPheCysGLYLeu 660
Db 2144 GGGAGGATGGAGACCGGTGATTCAGTGCAGCAAAACATGATGTGTCTGTGATTTCTTA 2203
Oy 661 LeuCysThrAsnLeuThrArgAlaProArg11eGLYGLN1eUValTYR11ePro 680
Db 2204 CTGCTGTACCATCTTACTCGAGCTCCACAGTATGTGTCACATTCAGAGGTGAGATCTTCCA 2263
Oy 681 ThrSerPheTYR11eGLN1YRVal11eAspCysSerGLYAlaH1SVal11eAsp 700
Db 2264 ACTTCCTTCTACATCAAAAGCCGGGTGATGTAGCTCAGTGGGCCATGTAGTTAGAT 2323
Oy 701 AspAspThrAspValGLYTYRValGLUAspGLYThrProCysGLYProSerMetCys 720
Db 2324 GATGATACGGATGTGGCTATGTAGAAATGGAAGCCCATGTGGCCCTTATGATGTGT 2383
Oy 721 LeuAspArgLYsCysLeuGLN11eGLN1AlaLeuAsnMetSerCysProLeuAspSer 740
Db 2384 TTACATGTGGAATCTCTTACAAATTCAMGCCCTTAATATGACAGCTGTCCATTCATTC 2443
Oy 741 LysGLYLYsValCysSerGLYH1SGLYValCysSerAsnGLUAlaThrCys11eCysAsp 760
Db 2444 AAGGTTAAAGTCTGTGGCGCATGGGTGTGTATGAAGCCACCTGCATTTGTGAT 2503
Oy 761 PheThrTRPAlaGLYThrAspCysSer11eArgAspProValArgAsnLeuH1SProPro 780
Db 2504 TTCACTCGGAGAGGACAGATTTGATCCGGGATCCAGTTAGAACCTTCACCCCCC 2563
Oy 781 LysAspGLUeUValProLYsGLYProSerAlaThrAsnLeu11e11eGLYSer11eAlaGLY 800
Db 2564 AAGATGAAGAGACCAAGAGGCTCTAGTCCACCAATCTCATTAATAGCTTCATCTGCTGT 2623
Oy 801 Ala11eLeuValAlaAla11eVal11eLeuGLYGLYThrGLYTRPG1YRPhelYsAsnValLYs 820
Db 2624 GCCATCTGTGAGAGCATGATGTCTTGGGGACAGAGCTGGGATTTAAAAATGTCAAG 2683
Oy 821 LysArgArgPheAspProThrGLN1GLYPro11e 832
Db 2684 AAGAGAGGTTTCATCTACTACAGCAAGGCCCATC 2719
RESULT 8
US-60-213-359-127
Sequence 127, Application US/60213359
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Deep, Dinu
TITLE OF INVENTION: Method for the identification of sequence polymorphisms using
TITLE OF INVENTION: Polynucleotide sequence databases, and single nucleotide poly
FILE REFERENCE: GX-0015 P

CURRENT APPLICATION NUMBER: US/60/213,359
: CURRENT FILING DATE: 2000-06-21
: NUMBER OF SEQ ID NOS: 7924
: SOFTWARE: PERL Program
: SEQ ID NO 127
: LENGTH: 6401
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID NO: 037502.4
US-60-213-359-127

Alignment Scores:
Pred. No.: 8,48e-301 Length: 6401
Score: 4540.00 Matches: 832
Percent Similarity: 99.88% Conservative: 0
Best Local Similarity: 99.88% Mismatches: 0
Query Match: 99.71% Indels: 1
DB: Gaps: 0

US-09-634-252a-4 (1-832) x US-60-213-359-127 (1-6401)

OY 1 MetLysPROProGlySerSerSerArgGlnProProLeuAlaGlyYCSerLeuAlaGly 20
Db 224 ATGAAGCCGCGCGGAGCAGCTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 283
OY 21 AlAserGlyGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
Db 284 GCTTCTCTGGGCG 343
OY 41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer 60
Db 344 AGCGCGCGCGCGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 403
OY 61 ArgProArgAlaTroglyValAlaAlaProSerAlaProHisTrpAsnGlnTrpAlaGlu 80
Db 404 CG 463
OY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100
Db 464 AAAAATTTGGAGCTCGCGCAGATGAAGCAATATTCACACAAAGCAATACACAGCAAT 523
OY 101 HisSerTyrSerAsnAlaMetGlnGlnGlnLeuProSerArgLeuIleTyrTyr 120
Db 524 ATCAGTTACAGCATCAATGCAAGAAAGAAATCACACTGCTTCACAGCTCATATATAC 583
OY 121 IleAsnGlnAspSerGlnSerProTyrHisValLeuAspThrLysAlaArgHisGln 140
Db 584 ATCAACCAAGACTCGGAAAGCCCTTATCAGCTTCTTGACAAAGCAAGCAACACAA 643
OY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160
Db 644 AAACATTAATTAAGCTGTGCATCTGCGCCAGCAAGCTTCCAGATGAAGCTTCGCTCC 703
OY 161 LysPheLeuLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGlnIle 180
Db 704 AAATTTATTTTACCTCATCTGACATGACAAATGCTTTGTCTTCTTGTATATGAGAA 763
OY 181 HisTyrGlnAsnGlyLysProGlnTyrSerLysGlyGlnHisCysTyrTyrHisGly 200
Db 764 CATACCAAAATGGGAACACACAGTACTTAAGGCTGGAGGCACTTTACTACATGGA 823
OY 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220
Db 824 AGCATGAGAGCGGCAAGCAAGCTCAAGTGGCTGTCAACCTGCAATGCACTTCATGCG 883
OY 221 MetPheGlnAspSerThrPheValTyrMetIleGlnProLeuGlnLeuValHisAspGlu 240
Db 884 ATGTTTAAAGATGATACCTTCTGTATATGATAGACCACTAGAGCTGGTTCATGATGAG 943
OY 241 LysSerThrGlyArgProHisIleIleGlnThrLeuAlaGlyGlnTyrSerLysGln 260

Db 944 AAAAGCAGAGTCGACCAATATATCCAGAAACCTTGGCAGGACAGTATCTAAGCA 1003
OY 261 MetLysAsnLeuThrMetGlnArgGlyAspGlnTyrProPheLeuSerGlnLeuGlnTyr 280
Db 1004 ATGAAGAAATCTCATATGAGAAAGAGGTGACAGAGTGGCCCTTCTCTCTGATATACAGTGG 1063
OY 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlnLeuLeuLysTyr 300
Db 1064 TTGAAAG 1123
OY 301 LeuGlnLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAla 320
Db 1124 TTGGAACCTTATGATTTGTTAATGATCAAAAGCTATTAAGACATCGCTCTCTCATGA 1183
OY 321 HisThrAsnAspPheAlaLysSerValAlaAsnLeuValAspSerIleTyrLysGlnGln 340
Db 1184 CATACCAACAACTTGGCAAGTCCGGGCAACCTTGTGATATCTTAACAAGAGCGAG 1243
OY 341 LeuAsnThrArgValValLeuValAlaValGluThrTrpThrGlnLysAspGlnIleAsp 360
Db 1244 CTCACACACAGGTTTCTCTGCTGCTGTAGAGACCTGGACCTGAGAAGATCAGATTGAC 1303
OY 361 IleThrThrAsnProValGlnMetLeuHisGlnPheSerLysTyrArgGlnArgIleLys 380
Db 1304 ATCACCACCAACCTTGGCAGATGCTCCATGAGTTCTCAAAATCCGCGCAGCCATTAG 1363
OY 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSer 400
Db 1364 CACATGCTGATGCTGTGGACCTTCATCTCGCGGCTGACATTTACATTAAGAACACAGT 1423
OY 401 LeuSerTyrPheGlyGlyValLysSerArgThrArgGlyValGlyValAsnGlnTyrGly 420
Db 1424 CTGAGTTACTTTGGAGGTGTCTGTTCGCCAAGAGAGAGTGTGTGATGATGATGTGT 1483
OY 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440
Db 1484 CTTCCAATGCGCAGGCGCAAGATATATTCGACAGGCTGTGCTCAAAACCTTGGATCCAA 1543
OY 441 TrpGlnProSerSerArgLysProLysCysAspCysThrGlnSerTrpGlyGlyCysIle 460
Db 1544 TGGCAACCTTCTAGACAAAGCCAAATGTGACGACAGATCTGGGGGCGCTGCATC 1603
OY 461 MetGlnLeuThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGlnTyr 480
Db 1604 ATGAGCAAAACAGGCGGTGCCATTCGAAATTTCAAAAGTCCACCATTTTGGAGTAT 1663
OY 481 ArgAspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsnArgProThrLysLeuPhe 500
Db 1664 AGAGACTTTTACAGAGAGAGAGGTGAGCTGCTTTTCAACAGGCCAACCAACCTATTT 1723
OY 501 GlnProThrGlnCysGlyAsnGlyTyrValGlnAlaGlyGlnLysCysAspCysGlyPhe 520
Db 1724 GAGCCACAGGAAATGTGAAATGATACGTGGAACCTGGGAGGAGTGTGATTTGCTTTT 1783
OY 521 HisValGlnCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540
Db 1784 CATGTGAGATCTTATGATTTATGCTGTAAGAAAGTTCCCTCTCCAAAGGGGCTCAGTGC 1843
OY 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGlnCys 560
Db 1844 AGCGAGCGGCGCTGCTGTAACTCAATACCTCATGCTTTTAAAGCCACGAGGATGAATG 1903
OY 560 SArgAspAlaValAsnGlnCysAspIleThrGlnTyrCysThrGlnLysAspSerGlnCys 580
Db 1904 CCGGAGTCTCTGGAAGAGAGTGTGATATTCGAATATTTGTTACTGAGACTCTGGTCACTG 1963
OY 580 SProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnArgCysTyr 600
Db 1964 CCCACCAATATCTTCAAGCAAGAGCGATATGCAATCAAAATTCAGGGGCGCTGCTGA 2023
OY 600 rAsnGlnLysCysLysThrArgAspAsnGlnCysGlnTyrIleTrpGlyThrLysAlaAl 620
Db 2024 CAATGGCGAGTGCAGAGACAGACAGACACACAGTGTGATACATCTGGGGAACAAAGGCTGC 2083

620 aglyseraspysphecystyrgrlulysleuasnhringlythrclulysglyasnycy 640
2084 AGGCTCTGACAAAGTCTGCTATGAAAGCTGAATACAGAGACAGACAGAGGAAACTC 2143
640 sglylaspyspglyspatgtrpiledincysserlyshisaspvalphcscglyphale 660
2144 CGGGAGAGATGAGACCGGTGATTCAGTCCAGCAAAACATGATGTCTGTGATGATTT 2203
660 uleucysrthrasnleuthrargalaprobrgileglylnleuglnclutletlapr 680
2204 ACTCTGACCAATCTTACTCGAGCTCCACGATATGCTCAACTTCAGGGAGATCAATCC 2263
680 otherSerPheThyHISglnGlyArgValIleaspCysSerGlyAlaHisValIleAsn 700
2264 AACTTCCTTCTACATCAAGGCGGGGTGATGTGACTGCTGATGCTGCTGCTGATTTAGA 2323
700 paspasphraspvalglytyrvalgluaspglythrProCysglyProserMetMeCy 720
2324 TGATGATACGGATGTGGGTATGTAGAAAGATGGAACGGCATGTGGCCGTCTATGATGTG 2383
720 sleuasparglyscysleuglnileglnleuasnmetSerSerCysProleuaspSc 740
2384 TTTACATCGGAAGTCTGCTCAAAATTCAMCCCTAAATATAGAGAGCTGTCTCCTCAATC 2443
740 rlysglylaspvalCysSerGlyHISglnGlyValCysSerasnGluAlaThrCysIleCysAs 760
2444 CAAGGTAAGTCTGCTGGGGCATGGGTGTGATATGAAGCCACCTGCTGCTGCTGCTGA 2503
760 ppherthrtrpalaaglythrAspCysSerIleargaspProvalArgAsnleuHisProp 780
2504 TTTCCCTCGGCGAGGACAGATGTGATCCGGGATCCAGTTAGGAACCTTCACCCCCC 2563
780 olyasppluglyprolysglyProserAlathrasnleuIleleGlySerIleAlaG 800
2564 CAAGATGAAGACCAAGGCTCTAGTCCACCAATCTCATATATAGGCTCCATCCCTG 2623
800 yalalleuValAlaAlaIleValIleuValIleuValIleuValIleuValIleuValI 820
2624 TGCCATCTCGTGAAGAGATGTGCTCTTGGGGGACAGCTGGGGATTTAAAAATGTCAA 2683
820 slysarargargPheaspProthrGlnGlnGlyProIle 832
2684 GAAAGAAAGTTGATCTCTACTACAGCAAGGCCCATC 2720

RESULT 9
US-09-760-484-15
Sequence 15. Application us/09760484
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT243
CURRENT APPLICATION NUMBER: US/09/760,484
CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 4440
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (4149)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (4219)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (4341)
OTHER INFORMATION: n equals a,t,g, or c
US-09-760-484-15

Alignment Scores:
Pred. No.: 1,1e-276 Length: 4440
Score: 4186.00 Matches: 759
Percent Similarity: 98.71% Conservative: 7
Best Local Similarity: 97.81% Mismatches: 10
Query Match: 91.94% Indels: 0
DB: 30 Gaps: 0

US-09-634-252a-4 (1-832) x US-09-760-484-15 (1-4440)

57 ALAAlaserSeraripProatrgAlaTTPGlyAlaAlaAlaProserAlaProHISTrpAsn 76
1 GCCGCCCTGCTCCGCCGCCGCCGCCCTGCGGGGCTCTGCGCCACCGCTCCCATTTGGAA 60
77 GluThrIaGluLysAsnleuGlyValIleuAlaspGluaspAsnThrleuGlnAsn 96
61 GAAACTGCAGAAAAAATTTGGAGTCTTGCAATGAGACAAATACATTCACACAGAT 120
97 SerSerSerasnIleSerTyfSerAsnAlaMetGlnIysGluIleThrleuProSerArg 116
121 AGCAGCAGTAATATACATTACAGCAATGCAATGCAAGAAATCACACCTGCTTCAAGA 180
117 LeuIleTyfTyfIleasnGlnaspSerGluSerProTyfHisValIleuaspThrLysAla 136
181 CTCATATATTACATCAACCAAGACTCGGAAAGCCCTTATACGTTCTTGACACAAGCA 240
137 ArgHISglnGlnLysHISasnLysAlaValIleuAlaspGlnAlaSerPheGlnIleGlu 156
241 AGACACGAGAAAAAATTAATAMGGCTGCTCATCTGGCCGAGAGCTTCCAGATTGAA 300
157 AlapheGlySerLysPheIleuAspLeuIleuasnAsnGlyLeuLeuSerSerasp 176
301 GCCCTGCGCTCAAAATTCATTCTTGACCTCATACTGAACAATGTTGTCTCTTGAT 360
177 TyfValGluIleHisTyfGluasnGlyLysProGlnTyfSerLysGlyGluHisCys 196
361 TATGTGAGATTCCTCAAGAAATGGAACACAGTACTTAAGGGTGAAGACACTGT 420
197 TyfTyfHisGlySerIleargGlyValIlyaspSerLysValIleuSerThrCysasn 216
421 TACTACCATGGAACATCAGAGCGCTCAAGACTCCAGAGTGGCTGTCTCAACCTGCAT 480
217 GlyLeuHISglnMetPheGluaspPThrPheValTyfMetIleGluProleuGluLeu 236
481 GCACTTCATGCAATGTTGAAGATGATTAACCTTCGTATATGATGAGACCACATGAGCTG 540
237 ValHisaspGluLysSerThrGlyArgProHisIleleGlnLysThrIleuAlaGlyln 256
541 GTTCATGATGAGAAAGACACAGGTGACACATATTAATCCAGAAACCTTGGCAGGACAG 600
257 TyfSerLysGlnMetLysAsnleuThrMetGluArgGlyaspGlnTyfProPheLeuSer 276
601 TATTTCTAGCAAAATGAAGATCTACATATGGAAGAGGTGACCGTGGCTTCTCTCT 660
277 GluLeuGlnTrpLeuLysArgArgLysArgAlaValAsnProserArgGlyIlePheGlu 296
661 GAATTACAGTGGTTGAAGAAGACAGACAGCACTGATCATCAGCGGTGATTTTGA 720
297 GluMetLysTyfLeuGluLeuMetIleValAsnAspHisLysThrTyfLysLysHisArg 316
721 GAAATGAAATATTTGGAACTTATGATGATTAATATACCAAAACGTTAAGAACATCGC 780
317 SerSerHisAlaHisThrAsnAsnPheAlaLysSerValValAsnleuValAspSerIle 336
781 TCTTCTCATGACACTTACCAACACTTTGCAAGAGTCCGTGCTGCACTTGTGATTTCTATT 840
337 TyfLysGlnGlnLeuasnThrArgValIleuValAlaValIleuValIleuValIleuVal 356
841 TACAGAGACAGCTCAACACAGCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
357 AspGlnIleaspIleThrThrAsnProvalGlnMetLeuHisGluPheSerLysTyfArg 376
901 GATCAGATTGACATCACCAACCCCTGTGAGATGCTCATGAGTTCTCAAAATATACCGG 960

QY 377 GlnArgIleLeuGlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyr 396
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 Db 961 CAGCCGATTAAACAGCATGCTGATGCTGGCACCCTATCTCGGGGAGACATTTCACTAT 1020
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 QY 397 LysArgSerSerLeuSerIlePheGlyValCysSerArgThrArgValGlyVal 416
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 Db 1021 AAGAGAGACAGTCTGATTAAGTCTGGAGGTCTGTTCTTCGCCAAGAGAGAGTGGTGTG 1080
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 QY 417 AsnGluTyrGlyLeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsn 436
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 Db 1081 AATGATATATGCTTCCCAATGGCAGTGGCACAAGTATATTCGACAGACCTGGCTCAAAAC 1140
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 QY 437 LeuGlyTleGlnTrpGluProSerSerArgLysProLysCysAspCysThrGlnSerTrp 456
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 Db 1141 CTGGAATCCCAATGGCAACCTTCTAGAGAAAGCCAAATATGACTGCACAGAAATCTCTGG 1200
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 QY 457 GlyGlyCysIleMetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSer 476
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 Db 1201 GGTGGCTGCATCATGAGAGAAACAGGGGTGCCCATTTCTCAAAATTTTCAAGTGCAGC 1260
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 QY 477 IleLeuGluTyrArgAspPheLeuGlnArgGlyGlyAlaCysLeuPheAsnArgPro 496
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 Db 1261 ATTTGGAGTATAAGACTTTTACAGAGAGAGTGGAGCTGCTTTTCAACAGGCCA 1320
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 QY 497 ThrIleLeuPheGluProThrGluCysGlyAsnGlyTyrValGluAlaGlyGluGluCys 516
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 Db 1321 ACAAGAGTATTGAGCCCAACGGAATGTGGAATGATGCGGAAGCTGGGAGAGAGTGT 1380
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 QY 517 AspCysGlyPheHisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsn 536
 |||||||
 Db 1381 GATGTGGTGTTCATGATGGAATGCTATGATGATATCTGTAAGAAATGTTCCCTCTCCAC 1440
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 QY 537 GlyAlaHisCysSerAspGlyProCysAsnAsnThrSerCysLeuPheGlnProArg 556
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 Db 1441 GGGGCTCACTCAGAGGAGCGGCCCTGCTGTACATACCTCTGCTTTTTCAGCCACGA 1500
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 QY 557 GlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAsp 576
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 Db 1501 GGGTGTGATGCCGGGATGCTGTGAACGAGTGTGATATGATATGATGCTGAGAGAC 1560
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 QY 577 SerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGln 596
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 Db 1561 TCTGCTCAGTGGCCCAATCTTCATATGACAAGAGGATGCAATGCAATCAAAATCCAG 1620
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 QY 597 GlyArgCysTyrAsnGlyLysLysThrArgAspAsnGlnCysGlnTyrIleTrpGly 616
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 Db 1621 GGGCCCTGCTACAAATGGCGAGTGCAGACACAGACACAGTGCAGTATCATCTGGGA 1680
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 QY 617 ThrLysAlaAlaGlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGlu 636
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 Db 1681 ACAAAAGCGTCAGAGGCTCACAAGTCTGCTATGAAGAGCTGAATACAGAAAGCACAGAG 1740
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 QY 637 LysGlyAsnCysGlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPhe 656
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 Db 1741 AAGGGAAATCGCGGAGAGATGAGAGACGGGTGATTCAGTGCAGCAAAACATGATGTCTTC 1800
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 QY 657 CysGlyPheLeuLeuLeuYstrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGly 676
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 Db 1801 TGTGGATTTCTTACTGTACCATCTTACTCGAGCTCCAGGTATGTGTAACCTCAGGGT 1860
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 QY 677 GluIleIleProThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHis 696
 |||||||
 Db 1861 GAGATCATTCACACTCTCTCTACCAATCAAGCGCGGTGATGTGACTGCAGGAGTGGCCAT 1920
 |||||||
 QY 697 ValValLeuAspAspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyPro 716
 |||||||
 Db 1921 GTAGTTTAAATATGATGATGAGATGTGGCTATGTAGACATGGAAGCCATGTGGCCG 1980
 |||||||
 QY 717 SerMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerCys 736
 |||||||
 Db 1981 TCTATGATGCTTTAGATGGGAATGCTCAAAATTCAGCCCTAAATATATAGAGAGCTGT 2040
 |||||||

QY 737 ProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThr 756
 |||||||
 Db 2041 CCACTCATTCACCAAGGTAAGTGTGTGGCCATGTGGGTGTACTAATGAAGCCACC 2100
 |||||||
 QY 757 CysIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsn 776
 |||||||
 Db 2101 TGCATTTGTGATTTTCACTGGCGAGGACAGATTGCAATATCCGGATCCAGTTAGGAAAC 2160
 |||||||
 QY 777 LeuHisProProLysAspGlyGlyProLysGlyProSerAlaThrAsnLeuIleGly 796
 |||||||
 Db 2161 CTTCACCCCCCAAGAGATGAAGAGACCCAAAGGATATGACACAGCAGCTAATAGGG 2220
 |||||||
 QY 797 SerIleAlaGlyAlaIleLeuValAlaIleValLeuGlyGlyThrGlyTrpGlyPhe 816
 |||||||
 Db 2221 GCGGTGGCGCCACCATTTCTGCGCTGGGGGTGATTTTGGAGGACAGCGGTGGGGAATA 2280
 |||||||
 QY 817 LysAsnValLysLysArgArgPheAspProThrGlnGlnGlyProIle 832
 |||||||
 Db 2281 GAAATGTCAAGAAAGAAAGAGTTGATCTACTCAGCAAGGSCCATC 2328
 |||||||
 Db 2281 GAAATGTCAAGAAAGAGTTGATCTACTCAGCAAGGSCCATC 2328
 |||||||
 RESULT 10
 US-60-360-207-15737
 : Sequence 15737, Application US/60360207
 : GENERAL INFORMATION:
 : APPLICANT: VENTER, J. Craig
 : TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 : FILE REFERENCE: CLO01321
 : CURRENT APPLICATION NUMBER: US/60/360, 207
 : CURRENT FILING DATE: 2002-03-01
 : NUMBER OF SEQ ID NOS: 47235
 : SEQ ID NO 15737
 : LENGTH: 2271
 : TYPE: DNA
 : ORGANISM: HUMAN
 : US-60-360-207-15737
 Alignment Scores:
 Pred. No.: 1,32e-258 Length: 2271
 Score: 3917.50 Matches: 714
 Percent Similarity: 96.05% Conservative: 16
 Best Local Similarity: 93.95% Mismatches: 25
 Query Match: 86.04% Gaps: 5
 DB: 80
 US-09-634-252A-4 (1-832) x US-60-360-207-15737 (1-2271)
 QY 29 ProAlaGlySerValProAlaSerAlaProAlaArgThrProProCysArgLeuLeu 48
 |||||||
 Db 4 CCGGCCGCGCGGTG-----CCGGCCGCGCGCGCGCGCTGCGCTGCTCTC 51
 |||||||
 QY 49 ValLeuLeuLeuLeuProProLeuAlaAlaSerSerArgProArgAlaTrpGlyAlaAla 68
 |||||||
 Db 52 GTCTTTCTCATGTAAGTCTGCTGCGCCTGCGCAGTCCGCGCGCGCGCGCGCT 111
 |||||||
 QY 69 AlaProSerAlaProHisTrpAsnGluThrAlaGluLysAsnLeuGlyValLeuAlaAsp 88
 |||||||
 Db 112 GCGGCCAGCGCGCTGCACTGGAATGAATCAACAAAAAACCTGGGAGTCTGCGCAGAT 171
 |||||||
 QY 89 GluAspAsnThrLeuGlnGlnAsnSerSerSer---AsnIleSerTyrSerAsnAlaMet 107
 |||||||
 Db 172 GAAGCAACACATTCACCAAAATATGACAGCAGCAAAATACAGTACAGCAGTCACTG 231
 |||||||
 QY 108 GlnLysGluIleThrLeuProSerArgLeuIleTyrTyrIleAsnGlnAspSerLeuSer 127
 |||||||
 Db 232 CAATAAGAAATACACCTCCCTTCAAGACTGTGTATCATCAACACAGACTCAAGAAAGC 291
 |||||||
 QY 128 ProTyrHisValLeuAspThrLysAlaArgHisGlnGlnLysHisAsnLysAlaValHis 147
 |||||||
 Db 292 CCTATTCATATGTTCTTGACACAAAGGCCAGACACCAACAGAAACAAATATAGCTGTGAT 351
 |||||||
 QY 148 LeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySerLysPheIleLeuAspLeuIle 167
 |||||||
 Db 352 CTGGCCAGGCAAGCTTCCAGATTCAGAGCTTTGCGGTCCAAAGTCAATTTGACCTCACA 411
 |||||||

Oy	168	LeuSnSnSnGnGLyLeuLeuSerSerAspPrYrValGluIleHnSTRGluSnGlyAsnGlyPro	187
Db	412	CTGAACAATGTTTGGCTATCTTCTGACTACGTGGAGATCCACTATGAAGAAGGGAAGAG	471
Oy	188	GlnTYrSerLysGlyGlyGluHnHScsTYrTYrHnSglSerIleArgGlyValLysAsp	207
Db	472	ATGTACTCTAAGGGGTGGAGACACCTGTTACTACACGGAAACATCAGAGGGCTCAGAT	531
Oy	208	SerLysValAlaLeuSerThrCysAsnGlyLeuHnSglYMetPheGluAspAspThrPhe	227
Db	532	TCCAGGGGGCTCATCGACTGCATGGAAATGACTGCATGGCAAGTTTGAAGAGACACCTTT	591
Oy	228	ValTYrMetIleGluProLeuGluLeuValHnAspGlyLysSerThrGlyARProHis	247
Db	592	GTAATATATGATAGAGACCTCTGGAACTGACTGATATATGAGAAAGACACAGCCGACCAAC	651
Oy	248	IleIleGlnLysThrLeuAlaGlyGlnTYrSerLysGlnMetLysAsnLeuThrMetLysIu	267
Db	652	ATAATCCAGAAACCTTGGCGAGGACAGTATTTCTAAGCAGATGAAGAATCTCAGACACAAAT	711
Oy	268	ArgGlyAspGlnTYrProPheLeuSerGluLeuGlnTYrPheLysARArgLysArgGlyAla	287
Db	712	GGCAGTGACCACTGGCCCTTCTGCTACCTGAATTTACAATGGCTGAGAGAAGAAAGAACGCG	771
Oy	288	ValAsnProSerARArgLysIlePheGluGlnMetLysTYrLeuGlnIleMetIleValAsn	307
Db	772	GTCATATCATCTCGTGGTGCTTTGAAGAAATGAAGTATTTTGGAGCTTATGATTTGTAAT	831
Oy	308	AspHisLysThrTYrLysLysLysHisArgSerSerHisAlaHisThrAsnAsnPheAlaLys	327
Db	832	GATACCAAGACGTTATGAAGAACACCCGCTTCTACAGGGCATACCACAACTTGGCANAAG	891
Oy	328	SerValValAsnLeuValAspSerIleTYrLysGlnIleAsnThnARValValLeu	347
Db	892	TCTGTGGTCACACTTGTAGATTCTATATTACAGAAGACGCTCAACACAGGGGTGTCTTG	951
Oy	348	ValAlaValGluThrTYrThrGluLysAspGlnIleAspIleThrThrAsnProValGln	367
Db	952	GTGGCTGCGAGACCTGGACCGAAGAGATACATTGCAATCACCATCAACCCGCTGACG	1011
Oy	368	MetLeuHnSglAspPheSerLysTYrArgGlnIleArgIleLysGlnHnSAlaAspAlaValHis	387
Db	1012	ATGTACTACTGACTTCTCCAACTACCAGCGAGGATCAACACAGCACGCTGACGCGGTCCAC	1071
Oy	388	LeuIleSerArgValThrPheHisTYrLysArgSerSerLeuSerTYrPheGlyGlyVal	407
Db	1072	CTCATCTCTCGCGCGATCTCCATTATGAAGAACACTGAGTACTTCTTGGAGCGGTG	1131
Oy	408	CysSerArgThrArgGlyValGlyValAsnGluTYrGlyLeuProMetAlaValAlaGln	427
Db	1132	TGTTCTGCAATAAAGGGGTGGTGGTGAATAGATGGTCTTCCAAATGGCGGTGGCACAA	1191
Oy	428	ValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTYrPgluProSerSerArgLys	447
Db	1192	GTAATTATCAGAGACCTGGCTCAAAACCTTGGAAATCCAGTGGAAACCTTCAGACAGAGAG	1251
Oy	448	ProLysCysAspCysThrGluSerTYrPglYcysIleMetGluGlnThrGlyValSer	467
Db	1252	CCAAATGTTGTAATCATAGACTCTCGGGCGCGCTGCATCATGAAGAAACAGGGGTGTCC	1311
Oy	468	HisSerArgLysPheSerLysCysSerIleLeuGlnTYrArgAspPheLeuGlnArgGly	487
Db	1312	CACCTCTCAAAAGTTCTCAAAATGCAGCATTTTGGAGTACAGAGACTTTTTCACAGAGAG	1371
Oy	488	GlyGlyAlaCysLeuPheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsn	507
Db	1372	GGCGAGAGCATCTCTTTCAATAGGCAACCTAAAGCTTTTGGACCCACAGCAATGTGGAAAT	1431
Oy	508	GlyTYrValGluAlaGlyGlnGluCysAspCysGlyPheHnSValGlnCysTYrGlyLeu	527
Db	1432	GGATATGTGGAGGCCGGGAGAGATTCGACATGTGGTTTCCATATGTGAATGCTATAGGACT	1491

OY	528	CyscyslvslvslvscysserleuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsn	547
Db	1492	TGCGTGAAGAAGTGTCCCTCCCTCCCAATGGGGCCCACTGCAGTGCAGGGCCCTGCTGTAC	1551
OY	548	AsnThrSerCysLeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCys	567
Db	1552	AACACCTCATCTCTTTTTCACGTCCACGAGGGCATATGAATGTCGGGATGTCCGTTAAACAGCTGT	1611
OY	568	AspIleThrGluTyrCysThrGlyAspSerGluGlnCysProProAsnLeuHisGlyGln	587
Db	1612	GATATCACCGAGTACTGCACCTGGAGACTCTGGCAGTGCACCCAGCAACCTTCATTAACAA	1671
OY	588	AspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyrAsnGluCysLysThrArg	607
Db	1672	GATGGCTATACCTGCATCAATCAAAATCAGGGCTGCTGTCAATATGGCGATGCAGACACAAG	1731
OY	608	AspAsnGlnCysGlnTyrIleThrGlyThrLysAlaAlaGlySerAspLysPheCysTyr	627
Db	1732	GACAATCATATCCAGTATCATCTGGGGGCAAAAGGCTCGGGGTCAAGCAAAATTCGTAT	1791
OY	628	GluLysLeuAsnThrGlnGlyThrGluCysGlyLysAsnGlyLysAspGlyAspArgTyr	647
Db	1792	GAAAGCTGACACAGGAAAGCACCAGAGAGGGCAATTGTGAAAGCATGCGAGACCGGTGG	1851
OY	648	IleGlnCysSerLysHisAspValPheCysGlyPheLeuLeuCysTrpAsnLeuThrArg	667
Db	1852	ATCCCGTGCACAGACATGATGTCTGTCTGTGATTTCTGCTTTCACACAAATCTTACCCGA	1911
OY	668	AlaProArgIleGlyGlnLeuGlnGlyCysIleIleLeuProThrSerPheTyrHisGlnGly	687
Db	1912	GCTCCACCTATTCGGTCAACTTCACAGAGATCATCCGACTTCTCTTATCATCAACAGGC	1971
OY	688	ArgValIleAspCysSerGlyAlaHisValIleLeuAspAspAspTrpAspValGlyTyr	707
Db	1972	CGAGTGAATGATCGTACAGTGGTGGTCACTGTATTTTACAGCATGATATACAGACGTGGTTAC	2031
OY	708	ValGluAspGlyThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGln	727
Db	2032	GTTGAAGATGGGACTCCCTGCGGCCCTCCCATGTATGTCTTAAGATCGAATGCTCTACAG	2091
OY	728	IleGlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGly	747
Db	2092	ATTCAAGCCCTGCATATATAGACGAGCTGCCCACTTGACTACAGGGTAAAGTGTCTCCGGC	2151
OY	748	HisGlyValCysSerAsnGluAlaThrCysIleCysAspPheThrTrrPalaGlyThrAsp	767
Db	2152	CACGGGGTGTATACACAGAACGCCACCTGCATCTGTGATTTCACTGTGGCGCAGCACAGAC	2211
OY	768	CysSerIleArgAspProValArgAsnLeuHisProProLysAspGluGlyProLysGly	787
Db	2212	TGCAGCATCCGGGATTCAGTTCGGAAACCCCAACCCCTTAAGATGAAGGCCCTTAAGGGT	2271
RESULT 11			
US-09-631-534-9			
: Sequence 9, Application US/09631534			
: GENERAL INFORMATION:			
: APPLICANT: Sheppard, Paul O.			
: APPLICANT: Balindur, Nand			
: APPLICANT: Deisher, Theresa A.			
: APPLICANT: Bishop, Paul D.			
: APPLICANT: Taft, David W.			
: TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP			
: FILE REFERENCE: 98-29C1			
: CURRENT APPLICATION NUMBER: US/09/631,534			
: CURRENT FILING DATE: 2000-08-03			
: PRIOR APPLICATION NUMBER: 60/092,371			
: PRIOR FILING DATE: 1998-07-10			
: PRIOR APPLICATION NUMBER: 60/147, 410			
: PRIOR FILING DATE: 1999-08-05			
: PRIOR APPLICATION NUMBER: 09/351,414			
: PRIOR FILING DATE: 1999-07-09			
: NUMBER OF SEQ ID NOS: 15			
: SOFTWARE: FastSeq for Windows Version 3.0			

SEQ ID NO 9
LENGTH: 4720
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2129)
NAME/KEY: misc_feature
LOCATION: (1)...(4720)
OTHER INFORMATION: n = A,T,C or G
US-09-631-534-9

Alignment Scores:
Pred. No.: 1,19e-253 Length: 4720
Score: 3851.00 Matches: 699
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 2
Query Match: 84.58% Indels: 0
DB: 24 Gaps: 0

US-09-634-252a-4 (1-832) x US-09-631-534-9 (1-4720)

OY 132 LeuAspThrLysAlaArgHisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAla 151
DB 27 CTTGACACAAAGGCAAGACACAGCAAAACATATATAGGCTGCTCCATCTGGCCAGGCA 86
OY 152 SerPheGlnIleGlnAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGly 171
DB 87 AGCTTCAGATTGAAGGCTTGCGCTCCAAATTCCTTCTGACCTCATACGAACATGGT 146
OY 172 LeuLeuSerSerAspLysValGluIleHisIleIleIleIleIleIleIleIleIleIle 191
DB 147 TTGTGCTCTCTGATATATGTGGAGATTCACACGAAATGGGAAACCACTACTCTAG 206
OY 192 GlyGlyGlnHisCysGlyTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAla 211
DB 207 GGTGGAAGGCACTTTACTACATGGAAGCATCAGAGCCGTCMAAGATCCAGAGTGGCT 266
OY 212 LeuSerThrCysAsnGlyLeuHisGlyMetPheGlnAspAspThrPheValIleIleIle 231
DB 267 CTGTCACCTCATGATGACCTTCATGGCATGTTGAAGATGATACCTGCTGATATGATA 326
OY 232 GluProLeuGlnLeuValHisAspGlnLysSerThrGlyArgProHisIleIleGlnLys 251
DB 327 GAGCCATAGAGCTGTCATGATGAGAAAGACAGGTCGACCAATTAATCCAGAA 386
OY 252 ThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMetGlnuArgGlyAspGln 271
DB 387 ACCTTGGAGGACAGATATTTAAGCAATGAAAGAAATCTCAGTATGGAAGAGGTGACAG 446
OY 272 TrpProPheLeuSerGlnuGlnIleIleIleIleIleIleIleIleIleIleIleIle 291
DB 447 TGGCCCTTCTCTCGAATTACAGTGTGAAAGAAAGAGACAGAGTGAATCCATCA 506
OY 292 ArgGlyIlePheGlnGlnMetLysTyrLeuGlnLeuMetIleValAlaAsnAspHisIle 311
DB 507 CGTGGATATTTGAAGAAATGAATATTTGGAACCTTATGATGCTATATGATCCAAAGC 566
OY 312 TyrLysLysHisArgSerSerHisAlaHisIleThrAsnAspPheAlaLysSerVal 331
DB 567 TATTAAGACATCGCTCTCTCTCTCATGACATACCAACAACCTTGCAAAAGTCCGTCGAC 626
OY 332 LeuValAspSerIleTyrLysGlnGlnLeuAsnThrArgValValLeuValAlaValGlu 351
DB 627 CTGTGGATTCATTTAACAAGGAGAGCTACACAGCGGCTTCTGCTGGCTGTAGAG 686
OY 352 ThrTTrpThrGlnLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGln 371
DB 687 ACCTGGACTGAGAGGATCAGATTGACATACCAACCAACCTGTCGAGATGCTCCAGAG 746
OY 372 PheSerLysTyrArgGlnArgGlnIleLysGlnHisAlaAspAlaValHisLeuIleSerArg 391
DB 747 TTCTCAAAATACGGCAGCGCATTAAGAGAGCATGCTGATGTCACCTCATCTCGCGG 806

OY 392 ValThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyValCysSerArgThr 411
DB 807 GTGACATTTCTACTATTAAGAACCACTGAGTTACTTTGAAGGTGTCTGTTCTCCACA 866
OY 412 ArgGlyValGlyValAsnGluTyrGlyLeuProMetAlaValAlaGlnValLeuSerGln 431
DB 867 AGAGAGATTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 926
OY 432 SerLeuAlaGlnAsnLeuGlyIleGlnIleIleIleIleIleIleIleIleIleIleIle 451
DB 927 AGCCTGCTCAAAACCTTGAATCCAAATGGGAACCTTCTAGCAGAAACCAAAATGTGAC 986
OY 452 CysThrGlnSerThrProGlyGlyCysIleMetGlnGlnIleIleIleIleIleIleIle 471
DB 987 TGCACAGAAATCTGGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1046
OY 472 PheSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGlyGlyValCys 491
DB 1047 TTTTCAAAAGTGACACATTTGGAGTATAGACCTTTTACAGAGAGAGGTGGACCTGC 1106
OY 492 LeuPheAsnArgProThrLysLeuPheGlnProThrGlnCysGlyAsnGlyTyrValGlu 511
DB 1107 CTTTTCACAGCCCAACAAAGCTATTGAGCCCAAGCAATGTGAATGGATACGTGGA 1166
OY 512 AlaGlyGlnGlyCysAspCysGlyPheHisValGlyCysTyrGlyLeuCysCysLysLys 531
DB 1167 GCTGGGAGAGAGTGTGATTTGTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1226
OY 532 CysSerLeuSerAsnGlyValHisCysSerAspGlyProCysCysAsnAsnThrSerCys 551
DB 1227 TGTTCCTCTCCCAAGGGGCTCAGTCAGCGAGCGGCGCTGCTGTACATATCTCAGT 1286
OY 552 LeuPheGlnProArgGlyTyrGlnCysArgAspAlaValAsnGlnCysAspIleThrGlu 571
DB 1287 CTTTTCACCCAGCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1346
OY 572 TyrCysThrGlyAspSerGlyCysProProAsnLeuHisLysGlnAspGlyTyrAla 591
DB 1347 TATTTGACTGGAGACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1406
OY 592 CysAsnGlnAsnGlnGlyArgCysTyrAsnGlyGlnCysLysThrArgAspAsnGlnCys 611
DB 1407 TGCATCAAAATCAGGCGGCTGCTCATGATGATGATGATGATGATGATGATGATGAT 1466
OY 612 GlnTyrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 631
DB 1467 CAGTACATCTGGGCAACAAAGCTGACAGGCTGACAAAGTTCTGCTATGAAAGCTGAAT 1526
OY 632 ThrGlnGlyThrGlnLysGlnCysGlyLysAspGlyAspArgTrpIleGlnCysSer 651
DB 1527 ACAGAGCGCACTGAGAGGGAACCTGCGGAGAGATGAGACCGGTGATTCAGTGCAGC 1586
OY 652 LysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIle 671
DB 1587 AAACATATGTTCTTCTGATTTCTACTGATCAATCTTACTGAGTCCACCTATTT 1646
OY 672 GlyGlnLeuGlnGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 691
DB 1647 GGTCACTTCAGGATGATTCACAACTCTTCAACCTCAACGAGCGGCTGATTTGAC 1706
OY 692 CysSerGlyAlaHisValValLeuAspAspAspThrAspValGlyTyrValGluAspGly 711
DB 1707 TGCAGTGTGCCCATGTATGTTTATGATGATATATACGATGATGATGATGATGATGAT 1766
OY 712 ThrProCysGlyProSerMetLeuLysLeuAspArgLysCysLeuGlnIleGlnAlaLeu 731
DB 1767 AGCCATGTGGCCGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1826
OY 732 AsnMetSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCys 751
DB 1827 AATATGACACAGCTGTCACCTCATTCACAAAGGTAAGTCTGTTGGGCGCATGGGTGTCT 1886

QY	752	Seqrsnsluialatrrcysilecyasppherhrrlplagllythrraspcysserilearg	771
Db	1887	AGTATGAAACCACCTGCATTTTGCGATTTCACCTGGGACGAGACAGATGAGTATCCGG	1946
QY	772	AspProValAlrgrasneuhisproprolylsaspisuglyprolysglyproserAlaIathr	791
Db	1947	GATCCACTTGAAGAACCTTCACACCCCCCAAGGATGAAGACCACCAAGGGTCATGGCCACC	2006
QY	792	AsnleuilellecgyserrileaglAlaIaleuValAlaAlaIleValleuGlyGly	811
Db	2007	AATTCATTAATAGGCTCCATGCGTGGGCCATCTCGTAGCAGCTAATGTCTTGGGCGC	2066
QY	812	ThrlgltprgIyPhelysasVallylsAsrIgrPheaspProthngInglngIyPro	831
Db	2067	ACAGGCTGGGAGTTTAAATAATGTCAAGAGAAGAGTTCCGATCTACTACGACAGGCGCC	2126
QY	832	Ile Ile	832
Db	2127	ATC	2129

```

RESULT 12
US-10-260-506-9
: Sequence 9, Application US/10260506
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Balindur, Nand
: APPLICANT: Balindur, Nand
: APPLICANT: Delsher, Theeresa A.
: APPLICANT: Bishop, Paul D.
: APPLICANT: Taft, David W.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE,
: FILE REFERENCE: 98-29C1, MAHP
: CURRENT APPLICATION NUMBER: US/10/260,506
: CURRENT FILING DATE: 2002-09-27
: PRIOR APPLICATION NUMBER: 60/092,371
: PRIOR FILING DATE: 1998-07-10
: PRIOR APPLICATION NUMBER: 60/147, 410
: PRIOR FILING DATE: 1999-08-05
: PRIOR APPLICATION NUMBER: 09/351,414
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 9
: LENGTH: 4720
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (3)...(2129)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(4720)
: OTHER INFORMATION: n = A,T,C or G
: US-10-260-506-9

```

Alignment Scores:	
Pred. No.:	1.19e-253
Score:	3851.00
Percent Similarity:	99.71%
Best Local Similarity:	99.71%
Query Match:	84.58%
DB:	43
	Gaps: 0
	Indels: 0
	Mismatches: 2
	Conservative: 0
	Matches: 699
	Length: 4720

US-09-634-252A-4 (1-832) x US-10-260-506-9 (1-4720)

OY	132	Leuasprrlrlysalaaarphiscinglnltyshiasnrllyalawahtslseualaginala	151
Dd	27	CTTGACACAAGGCAAGACACCAGCAAAAATPAATAAAGCGTGTCCATCTGGCCACAGCA	86
OY	152	SerPhesginnlegialalaPheciylserlyssphellileuaspheutlleleasnaasnely	171
Dd	87	AGCTTCACAGATTGAAGCCTTCGGCTGCCAAATTCATTCTTGACTCCTAACAGAACAATAGST	148
OY	172	LeuleuSerSerapTyValcIuultlehlstYrgluasnclylsbpProclntYrSerElys	:91

Db	147	TTGTTGTCCTTCGATTATATGAGATTCACTACGAAATAGGGAACACAGTACTTAAAG	206
Qy	192	GLYGLYGLNHISCYSTYRTRYRHISGLYSERILEARGLYVALYLLYASPERLYSVALA	211
Db	207	GGTGAGAGACACTGTTACTACCATGGAGACATCAGAGCGGTCAAGACTCCAAAGATCGAGCGCT	266
Qy	212	LEUSERTRYCYASNGLYLEUHSGLYMETPHEGLUASPASTPHRYVALTRYMETILE	231
Db	267	CTGTCAACCTGCAATGAGACTTCATGCGATTTGGAAGATGATACCTTCGTGTATGATCA	326
Qy	232	GLUPROLEUGLULEUVALHISAPGILYUSSERTHGLYARGPROHISTILEGILNLYS	251
Db	327	GAGCCACATGACCTGGTTTCATGATGAGAAACACAGCGTCGACACATATTAATCCAGAAA	386
Qy	252	THIRLEUALAGLYGINTYRSETRYSGLIMETLYSASILEUETHRMETGLIURARGLYASPGIN	271
Db	387	ACCTTGGCAGACAGACATATTCTAAGCAATGMAAATCTCACTATGGAAGAGGTGACACAG	446
Qy	272	TRPROPHLEUSERGLULEUGLINTPRILEUYSARGARYLSARGVALAVALASPROSER	291
Db	447	TGGCCCTTCTCTCGAATTACAGTGGTTGAAAGAAGCAAGAGACAGTGAATCCATCA	506
Qy	292	ARGGLYILERPHGLUGLUMETLYSTRILEUGLULEMETILEVALSNASPHISLYSTR	311
Db	507	CGTGATATATTTGAAAGAAATGAAATATTTTGGAACCTTATATTTGGTATATGATCA	566
Qy	312	TYRLVLSYHISARGSERSERHISALAHISSTRASASPHEALALAYSSERVALASIN	331
Db	567	TATAGAGACATCGCTCTTCATGCACATACCACAACTTTGCAAAAGTCGCGTGCAC	626
Qy	332	LEUVALASPSERILETRYLYSGLUGLILEUASNTRHARGVALALEUVALALAYALGLU	351
Db	627	CTTGAGGATTCATATTTACAGAGAGCGTCAACACCAGAGGTGTCTCGTGCGCTGTAAG	686
Qy	352	THIRPRPHGILYASPGINTILEASPILETHTHASPVALGIMETLEUHSGLU	371
Db	687	ACCTGACAGCAAGACATCAGATTGACATCCACCACCACTTCGTGAGATGCTCCATGAC	746
Qy	372	PHESELYSTRYARGGLINARGILEUYSGINHISALIASPALAYALHISLEULIESERARG	391
Db	747	TTTCTCAAAATACCGGCAGCGCATTAAGCAGCATCGTGAATGCTGTGCACCTCATCTGGCG	806
Qy	392	VALTRPHEHISTRYLYSARGSERLEUSERTRYRPHGLYGLYVALCYSSERATRYTHR	411
Db	807	GTGACATTTCACTATTAAGAGAGACAGTGTGAGTTACTTTGAAGGTGTCTGTCTCGCAC	866
Qy	412	ARGGLYVALGLYVALASNGLUTRYGLILEUPROMETALAYALAGLIVALLEUSERGIN	431
Db	867	AGAGAGATGGGTGATAGTAGATGCTTTCCAAATGGCAGTGCACACATATTATTCGACG	926
Qy	432	SERLEUUALAGLNASNLEUGLYLEGINTRPGILUPROSERSERARGYSPROLYSCYASAP	451
Db	927	AGCTTGCGCTCAAAACCTTGGAATCCAAATGGAAACCTTTAAGCAGAAAGCCAAATAATGAC	986
Qy	452	CYSTHRGLUSERTRYRGLYGLYCYSLIEMETGLUGLUTHRGLYVALSERHISSEARGLYS	471
Db	987	TGCACAGAAATCCTGGGGTGGCGTCGATCAGGAGGAAACAGGGGTGCCCATTCGCAAA	104
Qy	472	PHESERLYSCYSSERILEUGLUTRYRARGASPHLEUGLINARGLYGLYGLYALAYCS	491
Db	1047	TTTTTCAAGTGCACGATTTTGACGATATAGAGACTTTTTCACAGAGAGAGGTGACGCTCG	110
Qy	492	LEUPHEASNARGPROTHRTRYLEUPHGLIUPROTHGILUCYSGLYASNGLYTRYRVALGLU	511
Db	1107	CTTTTCAACAGGCAACAAGCTATTTTGAGCCACCGAATGTGGAAATGATACGTGGAA	116
Qy	512	ALAGLYGLUGLUCYASPCSYGLYPHEHISVALIGLYCYSTRGLYLEUCYSCYLSYLS	531
Db	1167	GCTGGGAGGAGATGTGTGTGTCTTTCATGTGGAAATGCTATATGCAATTAATGCTGTAA	122
Qy	532	CYSSETRLEUSERASNGLYALAHISCYSSERASPGILYPROCYSCYASNASNTRHSE	551

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Db      1227 TGTCCCTCTCCACGGGGCTCACTGCAGCGAGCGGCCCTGCTGTAACAATACCTCATGT 1286
OY      552 LeuphegInProArGgLyTyrgLUCysArGAsPaLaVaLaSngLUCysAsPLeThrgLu 571
      |||||||
Db      1287 CTTTTTCAGCCACGAGGATGAAATGACCGGATGCTGTAACGAGGTGATATTACTGAA 1346
OY      572 TyrcysThrgLyAsPserGlyGInCysProProAsnLeuHisLysGlnAspGlyTyraLa 591
      |||||||
Db      1347 TATTGTACTGAGACTGTGGTAGTGCCCAACAATCTTCATAGCAGACGATATGCA 1406
OY      592 CysAsngInAsngInGlyArGcSTyrAsngLyGluCysLysThrArGAsPAsngInCys 611
      |||||||
Db      1407 TGCATTCAAATCAGAGCGCGCTGCTACATGGCGAGTGCAGACAGACACAGTGT 1466
OY      612 GlnTyrlIetrgGlyThrLysAlaAlaGlySerAsPlysPheCysTyrgLulysLeuAsn 631
      |||||||
Db      1467 CAGTACATCTGGGGAACAAGGCTGAGAGTGTGACAAAGTTCTGCTATGAAAGCTGAAT 1526
OY      632 ThrGluGlyThrGluLysGlyAsnCysGlyLysAspGlyAsPaArgTrpIleGlnCysSer 651
      |||||||
Db      1527 ACAGAGGCACTGAGAGAGGAAGAACTCGGGAGAGATGAGACCGGTGATTCAGTCCAGC 1586
OY      652 LysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIle 671
      |||||||
Db      1587 AAACATGATGTGTTCTGTGGATTCTTACTGTACCAATCTTACTCGAGCTCCAGTATT 1646
OY      672 GlyGlnLeuGlnGlyGluIleIleProThrSerPheTyrlHisGlnGlyArgValIleAsp 691
      |||||||
Db      1647 GGTCACACTGAGGGTAGATCAATTCCAACTTCCTTACCATCAAGCGCGGTGATTGAC 1706
OY      692 CysSerGlyAlaHisValLeuAsPaSPThrAspValGlyTyraGluAspGly 711
      |||||||
Db      1707 TGCAGTGTGCCCATGTAGTTTAGATGATGATACGATGTGGGCTATGTAGAAAGATGA 1766
OY      712 ThrProCysGlyProSerMetMetCysLeuAsPaRgLyCysLeuGlnIleGlnAlaLeu 731
      |||||||
Db      1767 ACGCATGTGGCCCGCTGTATGATGTGTAGATCGGAAGTGGCTTCAATTCACAGCCCTA 1826
OY      732 AsnMetSerSerCysProLeuAsPserLysGlyLysValCysSerGlyHisGlyValCys 751
      |||||||
Db      1827 AATATGACCACTGTCCACTCGATTCCAAAGGTAAAGTCTGTTCGGCCATGGGCTGTGT 1886
OY      752 SerAsngLuAlaThrCysIleCysAsPheThrTrpAlaGlyThrAspCysSerIleArg 771
      |||||||
Db      1887 AGTAATGAAGCCACCTGCATTGTGTATTCACCTGGGCGAGACAGATTGCAGTATCCGG 1946
OY      772 AsproValArgAsnLeuHisProProLysAspGluGlyProLysGlyProSerAlaThr 791
      |||||||
Db      1947 GATCCAGTTAGGAACCTTCACCCCCCAAGAGATGAAGACCAAGGCTCTAGTGCACC 2006
OY      792 AsnLeuIleIleGlySerIleAlaGlyAlaIleLeuValAlaAlaIleValLeuGlyGly 811
      |||||||
Db      2007 AATTCATATATAGGCTCCATCGCTGTGTCATCTGTAGCAGCTATTGTCTTG6GGGC 2066
OY      812 ThrGlyTrpGlyPheLysAsnValLysLysArgArgPheAsPProThrGlnGlnGlyPro 831
      |||||||
Db      2067 ACAGGCTGGGGAATTAAATGTCAGAGAGAGAGTTCATCTACTCAGCAAGGCCCC 2126
OY      832 Ile 832
      |||
Db      2127 ATC 2129
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Search completed: June 1, 2003, 20:13:49
Job time : 4610 secs

Qy	21	AlAserCysglYProGlnarGgLYProAlaGlySerValProAlaSerAlaProAlaIarg	40
Db	130	GCCTCCGCGGGCCCCCAACCGGGCCCCCGGGCGGGCTGGCTGGCCACCGCCCCGGCCG	189
Qy	41	ThrProProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer	60
Db	190	ACGGCGCCGCGCGCGCTTCTGCTGCTTCTGGCTGGCTCGGCTCGCGCTCGCTCTCC	249
Qy	61	ArgProArgAlaTSPGlyAlaAlaAlaProSerAlaProHisTTPaSnGluThrAlaGlu	80
Db	250	CGGGCCCCGGCGCTGGGGGGCGTGGCGGCCCGACGGCTCGCATTTGGAAATGCAGAA	309
Qy	81	LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn	100
Db	310	AAAAATTGGAGAGCTGGCGAGATGAAGACAAATTCATTGCATTAACAGAAATAGCAGAGTAAT	369
Qy	101	ILeserTYrSerAsnAlaMetGluLysGluLeuThrLeuProSerArgLeuIleTYrTYr	120
Db	370	ATCGATTACACAAATTCGATCGATCGAAGAAATTCACACTGGCTTCAAGACTCATATTATAC	429
Qy	121	ILeasnglnAspSerGlnSerProTYrHisValLeuAspThrLysAlaArgHisGlnGln	140
Db	430	ATCAACCAAGACCTGGAAAGCCCTTATCAGCTTCTTGACACAAAGCAAGCACACAGCAA	489
Qy	141	LysHisAsnLYsAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer	160
Db	490	AAACCTAATAAGCGCTGCATCTCGGCCCGACGCAACCTTCCAGATTGAAGCCTTGCGCTCC	549
Qy	161	LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTYrValGluIle	180
Db	550	AAATTCAATCTTGACCTCATACTGAAACAATGGTTGGTGTCTTCGATTATGTGGAGATT	609
Qy	181	HisTYrGluAsnGlyLysProGlnTYrSerLysGlyGlnHisCysTYrTYrHisGly	200
Db	610	CACCTACGAAATGGGGAACACACAGTACTTAAGGGGTGGAGACACTGTACTACCATCATGA	669
Qy	201	SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly	220
Db	670	ACCATCAGAGGGGTCAAAACATCCAAAGGGGTCTGTCAACTGCAATGAGACTTCAATGAGC	729
Qy	221	MetPheGluAspAspThrPheValTYrMetIleGluProLeuGluLeuValHisAspGlu	240
Db	730	ATGTTTGAAGATGATACCTCTCTGTATATGATAGAGCCACTGAGCTGGTTCATGATGAG	789
Qy	241	LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTYrSerLysGln	260
Db	790	AAAAGACAGCGTCGACACCATATTAATCCGAAAAACCTTGGCGAGACAGATTCTTAAGCAA	849
Qy	261	MetLysAsnLeuThrMetGluArgGlyAspGlnTTPProPheLeuSerGluLeuGlnTTP	280
Db	850	ATGAAACAAATCTCACTATGGAAAGAGGTGACCAAGTGGCCCTTCTCTCTTAATTTACAGTGG	909
Qy	281	LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGluGluLeuMetLysTYr	300
Db	910	TTGAAAAAGAGAGAGACAGCATCATCATCAGTGTATATTGTAAGAAATTAAT	969
Qy	301	LeuGluLeuMetIleValAsnAspHisLysThrTYrLysLysHisArgSerSerHisAla	320
Db	970	TTTGAACTTATGATGTGTATATGATTCACAAACCGTATTAAGACAGATCGCTTCTCTACGCA	1029
Qy	321	HisThrAsnAsnPheAlaLysSerValLysLeuValAspSerLetyrLysGluGln	340
Db	1030	CATACCAACCAACTTTCGAAAGTCCGGTGCACACTTGTGGATTCTAATTTCACAGGACGAG	1089
Qy	341	LeuAsnThrArgValValLeuValAlaValGluThrTTPThrGluLysAspGlnIleAsp	360
Db	1090	CTCAACACCAAGGGTTGTCTGGTGGCTGTAGAGACCTGGACATGAGAGATCGATTGAC	1149
Qy	361	IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTYrArgGlnArgIleLys	380
Db	1150	ATCAGACCAACACCTGGCGAGATGCTGCATAGAGTCTCAAAATTAACGGGACGCATTAAG	1209
Qy	381	GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTYrLysArgSerSer	400

Db	1210	CAGCATGCTGATCTGTGGACACCTCATCTCCGGGTGACATTTCATTAAGACAAGCAGT	1269
QY	401	LeuSerTyrPheGlyGlyValCysSerArgThrArgGlyValGlyValAsnGluTyrGly	420
Db	1270	CTGAGTACTTCTGGAGGTCTCTGTTCTCCGACACAGAGAGAGTTGGTGTGAATGATAGGT	1329
QY	421	LeuProMetAlaValAlaGluValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln	440
Db	1330	CTTTCATATGCGACAGGCGCACAGATTATATCGAGAGCCTGGCTCAAAACCTTGGAAATCCAA	1389
QY	441	TripGluProSerSerArgLysProLysCysAspCysThrGluSerTyrGlyGlyCysIle	460
Db	1390	TGGGAACCTCTAGACAAAGCCAAATGTGACTGCACAGAAATCTGGGCTGGCTGCATTC	1449
QY	461	MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr	480
Db	1450	ATGAGAGCAAAACAGGGCTGTCCCATTTCCGAAAATTTTCMAAGTCAGCATTTTGGAGAT	1509
QY	481	ArgAspPheLeuGluIleArgGlyGlyGlyValAcysLeuPheAsnArgProThrLysLeuPhe	500
Db	1510	AGAGACTTTTACAGACAGACAGAGGTGGAGCCTTCCTTTCAACAGGCCAACAAAGCTATTT	1569
QY	501	GluProThrGluCysGlyAsnGlyTyrValGluAlaGlyGluGluCysAspCysGlyPhe	520
Db	1570	GAGCCCAACGGAATGTGGAATGATGATACGTGGAGACGTGGGAGAGTGTGATGTGTGTTT	1629
QY	521	HisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyValHisCys	540
Db	1630	CATGTGGATGCTTATGATTTATGCTGTGAAGAAATGTCCCTTCACAGGGGCTCACTGC	1689
QY	541	SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGluCys	560
Db	1690	AGCGAGGGGCTGCTGTAAACATACCTCATCTCTTTTACACCACAGAGGTATGATATGC	1749
QY	561	ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCys	580
Db	1750	CGGATGCTGTGAACGAGTGCATATTACTGAATATTGTACTGGAGACTCTGTGCTAGTGC	1809
QY	581	ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGluTyrProCysTyr	600
Db	1810	CCACCAAAATCTCTCAAAACCAACGGAATATGATCAATCAAAATTCAGGGGCGGTGCTAC	1869
QY	601	AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleLeuProGlyThrLysAlaAla	620
Db	1870	AATGGCGAGTGCACACACAGACACCAACAGTGTCACTGATCTGGGAAACAAAGCTGCA	1929
QY	621	GlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGluLysGlyAsnCys	640
Db	1930	GGGTGTGACAAAGTCTGCTATGAAAAGCTGAATACAGAGGCACTGAGAAAGGAAACTGC	1989
QY	641	GlyLysAspGlyAspArgTrrPrlIleGlnCysSerLysHisAspValPheCysGlyPheLeu	660
Db	1990	GGGAAGATGGAGACCGGTGATTCAGTCCAGCAAAACATGATGTCTTCTGTGATTTCTTA	2049
QY	661	LeuCysThrAsnLeuThrArgAlaProArgIleGlyGluLeuGlnGlyGluIleIlePro	680
Db	2030	CTCTGTACCAATCTTACTGTGAGCTCCACGATTTGGTCAACTTCAGGGGTGAGATTCCTCA	2109
QY	681	ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyValHisValValLeuAsp	700
Db	2110	ACTTCCTTCTACCAATCAAGCGGGGTGATTGACTGCAGTGGTCCCATGTAGTTTATGAT	2169
QY	701	AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys	720
Db	2170	GATGATACCGAGTGTGGCTATGTAGAAGATGAGAACCCATGTGGCCCGCTTATGATGTGT	2229
QY	721	LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer	740
Db	2230	TTAGATCGGAAGGTCTTACAAATTCAGCCCTTAATATGACAGCTGTCCACATCGATTCC	2289
QY	741	LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp	760

Db 2290 AAGGTAAGTCTGTTCGGCCATGGGCTGTACTAATGAAGCCAGCTGATTTGTGAT 2349
Qy 761 PheHrTPAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisPropo 780
Db 2250 TTCACCTGGGAGGAGACGATTTGCAGTATCCGGATTCAGTACAGCTTACACCCCCC 2409
Qy 781 LysAspGlyGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
Db 2410 AAGATGAAGGAGCCCAAGGCTCTAGTGCACCAATCTCATTAATAGGCTTCATCGCTGT 2469
Qy 801 AlalleuValAlaAlaIleValleuGlyGlyThrGlyTyrGlyPheLysAsnValLys 820
Db 2470 GCCATCCGAGGAGCGCTATTGTCTTGGGGGACAGGCTGGGATTTAAAAATGTCAG 2529
Qy 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832
Db 2530 AAGAGAGCTTCGATCTACTACAGCAAGCCCATC 2565

RESULT 2
US-10-126-052A-149
: Sequence 149, Application US/10126052A
: GENERAL INFORMATION:
: APPLICANT: Mutray, Richard
: APPLICANT: Aziz, Natasha
: APPLICANT: Eos Biotechnology, Inc.
: TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
: TITLE OF INVENTION: Methods of Screening for Modulators of Lung Cancer
: FILE REFERENCE: 018501-001530US
: CURRENT APPLICATION NUMBER: US/10/126, 052A
: CURRENT FILING DATE: 2002-04-18
: PRIOR APPLICATION NUMBER: US 60/284, 770
: PRIOR FILING DATE: 2001-04-18
: PRIOR APPLICATION NUMBER: US 60/290, 492
: PRIOR FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: US 60/339, 245
: PRIOR FILING DATE: 2001-11-09
: PRIOR APPLICATION NUMBER: US 60/350, 666
: PRIOR FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US 60/334, 370
: PRIOR FILING DATE: 2001-11-29
: PRIOR APPLICATION NUMBER: US 60/372, 246
: PRIOR FILING DATE: 2002-04-12
: NUMBER OF SEQ ID NOS: 691
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 149
: LENGTH: 3054
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-126-052A-149

Alignment Scores:
Pred. No.: 0 Length: 3054
Score: 4553.00 Matches: 832
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-634-252A-4 (1-832) x US-10-126-052A-149 (1-3054)

Qy 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20
Db 224 ATGAGAGCGCGCGGAGAGCTCGCGGAGCGCGCGCTGGCGGCTGCAGCTTCGCGGCG 283
Qy 21 AlAserCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
Db 284 GCTTCCTGGGCGGCGGCGGAGCGGCGCGCTGGCGGCTGCAGCGCGCGCGCGCGCGC 343
Qy 41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer 60
Db 344 ACGCGCGCGCGCGCGCTTCCTTCCTTCGCGGCGCGCTGCAGCGCGCGCGCGCGCTGC 403
Qy 61 ArgProArgAlaTyrGlyAlaAlaAlaProSerAlaProHisTyrAsnGlnThrAlaGln 80

Db 404 CGGCCCCGCGCGCGGCGGCGCTGCTGCGCCAGCGCTCCGATTCGATGAATGAACATGCAGAA 463
Qy 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100
Db 464 AAAAATTTGGAGTCTCGCGAGATGAAGACAAATTCATTCGACAGATTAACAGCAGTAAT 523
Qy 101 IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrTyr 120
Db 524 ATCAGTTACAGCATGCATGCAGAAAGAAATACACACTGCTTCAGACTCATATATATAC 583
Qy 121 IleAsnGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaArgHisGlnGln 140
Db 584 ATCAACCAAGACACTCGGAAAGCCCTTATCACGTTCTTGACACAAAGGACAGACACAGCAA 643
Qy 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGlnAlaPheGlySer 160
Db 644 AAACATTAATTAAGGCTGTCTGATCTGGGCCAGGCAAGCTTCAGATTAAGGCTTCGCGCTCC 703
Qy 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIle 180
Db 704 AAATTCATTCTTACCTCATCTGACATGAACAAATGTTTGTCTCTCTGATTTATGTGGAGATT 763
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Qy 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220
Db 824 AGCATGAGAGGCTCAAGAGCTCAAGGCGCTGTCAACCTGCAATGAGCTTCATCAGGC 883
Qy 221 MetPheGluAspAspThrPheValTyrMetIleGluProLeuGluLeuValHisAspGlu 240
Db 884 ATGTTTGAGATGATATACCTTCGCTGATATATAGACCACTAGACGTGCTCATGATGAG 943
Qy 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260
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Qy 261 MetLysAsnLeuThrMetGluGluGlyAspGlnTyrProPheLeuSerGluLeuGlnTyr 280
Db 1004 ATGAAGAATCTCACTATGCAAGAGAGTGACCACTGGCCCTTCTCTCTGAAATTAACATGG 1063
Qy 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGluGluMetLysTyr 300
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Db 1124 TTGGAATCTATGATGTATGATATGATCAAAAACGTATGAAGATCGCTCTTCATGACA 1183
Qy 321 HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGluGln 340
Db 1184 CATACCAACAACCTTTCAAAGTCCGTCGTCACCTGTGTGATTTCAAGAGACAG 1243
Qy 341 LeuAsnThrArgValValLeuValAlaValGlnThrTyrThrGluLysAspGlnIleAsp 360
Db 1244 CTCACACCAAGGTTTCTGCTGGTGGCTGTAGAACCTGGAGCTAGAAAGATTCAGATTGAC 1303
Qy 361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIleLys 380
Db 1304 ATCACCACCAACCCCTGTGAGATGATCATGATTTCAAAAATACCGGAGCCATTAAG 1363
Qy 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSer 400
Db 1364 CAGCATGTGATGCTGTGACCTCATCTCGGGGTGACATTTACATTAAGAAAGACAGT 1423
Qy 401 LeuSerTyrPheGlyGlyValCysSerArgThrArgGlyValGlyValAsnGluTyrGly 420
Db 1424 CTGAGTTACTTGGAGGTGTCTTCTTCGACAAAGAGATTTGTGTGAATGATGATGCT 1483
Qy 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440

1484 CTTCCAAATGGCAGTGGCACAACTATTATCGAGACCTGGCTCAAAACCTTGGAAATCCAA 1543
OY 441 TFGTuproSerSerArglyProlyscysAspCysThrGluSerTrpIleGlycysIle 460
DB 1544 TGGGAACCTTCTAGCAGAAAGCAAAATGTGACTGCACGATCTCGGGCTGGCTGCATC 1603
OY 461 MetGluGluThrGlyAlaSerHisSerArglyPheSerLysCysSerIleLeuGluIlyr 480
DB 1604 ATGGAGGAAACAGGGGTGTCCATTCTCGAAAATTTTCAAAATTCAGACGATTTTGGAGTAT 1663
OY 481 ArgAspPheLeuGlnArgIleGlyGlyAlaCysLeuPheAsnArgProThrLysLeuPhe 500
DB 1664 AAGGACTTTTTCACAGAGAGAGAGTGGAGCTGCTCTTTTCAACAGGCCAACAAAGCATTTT 1723
OY 501 GluProThrGluCysGlyAsnGlyTyrrValGluAlaGlyGluGluCysAspCysGlyPhe 520
DB 1724 GAGCCACGCAATGTGGAATGATGATCGGAAGCTGGGAGAGAGATGATGATGATGATGAT 1783
OY 521 HisValGluCysTyrrGlyLeuGlyCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540
DB 1784 CATGTGGAAATGCTATGGATTATGCTGTAAAGAAATGTTCCCTCCACAGGGGCTCATCTGC 1843
OY 541 SerAspGlyProCysCysAsnThrSerCysLeuPheGlnProArgGlyTyrrGluCys 560
DB 1844 ACGGAGGGGCTCGCTGTAACATACCTATGCTTTTTCAGCCAGAGGATATGATGC 1903
OY 561 ArgAspAlaValAsnGluCysAspIleThrGlyTyrrCysThrGlyAspSerGlyGlyCys 580
DB 1904 CGGAGATGCTGTGAAACAGTGTGATTTACTGAAATATTTGACTGGAACACTGCTGCTAGTGC 1963
OY 581 ProProAsnLeuHisLysGlnAspGlyTyrrValCysAsnGlnAsnGlnGlyArgCysTyrr 600
DB 1964 CCACCAATCTTCTATAGCAAGACGATATGCTGCAATTCAAATATCAAGGCGCTGCTAC 2023
OY 601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrrIleTrpGlyTyrrIleVala 620
DB 2024 AATGGCAGTGGCAAGACCAAGACCAACCAAGTGTCACTACATCTGGGGAACAAAGCTGCA 2083
OY 621 GlySerAspLysPheCysTyrrGlyLeuAsnThrGluGlyThrGlyGlyGlyAsnGlyCys 640
DB 2084 GGGTCTGACAAAGTCTGCTATGAAAGCTGAATATACAGAAAGGCACTAGAGAGGAAACTGC 2143
OY 641 GlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660
DB 2144 GGGAGAGATGGAGACCGGTGATTCAGTGCAGCAACATGATGATGATGATGATGATGAT 2203
OY 661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyGluIleIlePro 680
DB 2204 CTCTGTACCAATCTTACTCGAGCTCCACGATTTGTCACCTTCAGGGGTGAGATCATTC 2263
OY 681 ThrSerPheTyrrHisGlnGlyArgValIleAspCysSerGlyAlaHisValIleLeuAsp 700
DB 2264 ACTTCTCTTACCATCAAGGCGGGGTGATTCAGTGCAGTGTGCTCCATGATGATGATGAT 2323
OY 701 AspAspThrAspValGlyTyrrValGluAspGlyThrProCysGlyProSerMetMetCys 720
DB 2324 GATGATAGCGATGTGGCTATGTAGAAGATGAAAGCGCATGTGGCCGTCTATGATGATGAT 2383
OY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740
DB 2384 TTGAGATCGGAAGTGCCTACAAATTCAGGCTTAAATATGAGCAGCTGTCCACGATGATCC 2443
OY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760
DB 2444 AAGGTAATATCTGTTGGGCGCATGGGCTGTAGTATGAAACCAACCTGCATTTGGAT 2503
OY 761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780
DB 2504 TTCACCTGGGCGAGGACAGATTCAGATTCGGGATCCAGTTAGGAACCTTCACCCCCC 2563
OY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
DB 2564 AAGGATAAAGACCAAGGCTCTAGTCCACCAATCTCATATATAGGCTCATCTGCTGCT 2623

OY 801 AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTrpGlyPheLysAsnValLys 820
DB 2624 GCCATCTGCTGAGCAGTATGTTCTTGGGGGACAGGCTGGGATTTAAAAATGTCAG 2683
OY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832
DB 2684 AAGAGAGGTTGATCTACTACTACGCAAGGCCCATC 2719
RESULT 3
US-10-126-052A-324
Sequence 324, Application US/10126052A
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Murray, Richard
TITLE OF INVENTION: Methods of diagnosis of Lung Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Lung Cancer
FILE REFERENCE: 018501-001530US
CURRENT APPLICATION NUMBER: US/10/126, 052A
CURRENT FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US 60/284,770
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/290,492
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 60/339,245
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/334,370
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 691
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 324
LENGTH: 3054
TYPE: DNA
ORGANISM: Homo sapiens
US-10-126-052A-324
US-10-126-052A-324 (1-832) x US-10-126-052A-324 (1-3054)
Alignment Scores:
Pred. No.: 0 Length: 3054
Score: 4553.00 Matches: 832
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9
OY 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20
DB 224 ATGAAAGCGCGCGGACGAGCTGCGGCGACCGCGCTGGCGGCTGCGAGCTTGGCGGC 283
OY 21 AlaSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
DB 284 GCTTCTGGGCGCCCAACGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 343
OY 41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuProProLeuAlaAlaSer 60
DB 344 ACGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
OY 61 ArgProArgAlaTrpGlyAlaAlaAlaProSerAlaProHisTrpAsnGluThrAlaGlu 80
DB 404 CGGCGCGCGCGCGCGGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463
OY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100
DB 464 AAAAATTTGGAGATCTCTGCGCAGATGAAGACAAATATTCGAACAGATAGCAGCACTAAT 523
OY 101 IleSerTyrrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrr 120

Dh 524 ATCAGTTACGACGAAATGCGAGAAAGAAATCAGACTGCGCTTCAGACTCATATATTTAC 583
Oy 121 ILeasnGlnAspSerGlnSerProTyrHisValIleuAspThrLysAlaArgHisGln 140
Dh 584 ATCAACCAAGACTCGGAAAGCCCTTATTCAGCTTCTTGACACAAAGGACAGACACACAA 643
Oy 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160
Dh 644 AAACATTAATTAAGGCTGTCCATCTGCGCCAGGCAAGCTCCAGATTGAGGCTTCGCGTCC 703
Oy 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerSplyValGluIle 180
Dh 704 AAATTCATTTCTTGACTCTGACTGAAACAATGTTGTCTCTCTCATTAATGCGAATT 763
Oy 181 HsTyrGluAsnGlyLysProGlnTyrSerLysGlyGluHisGlyTyrTyrHisGly 200
Dh 764 CACTACGAAATGGGAAACACAGTACTTAAGGGTGGAGAGACAGCTTCTACCAATGCA 823
Oy 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220
Dh 824 ACCATCAGAGGCGTCAAAAGACTCCAGAGTGGCTCTGTCAACCTGCAATGCACTTCAAGC 883
Oy 221 MetPheGluAspAspThrPheValTyrMetIleGluProLeuGluLeuValHisAspGlu 240
Dh 884 ATGTTTGAAGATGATACCTTCGTGATATGATAGACCCTAGAGCTGGTTTCATGAGAG 943
Oy 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260
Dh 944 AAAGACAGCGTGCAGACCATATTAATCCAGAAACCTTGGCAGACAGTATTTCAACAA 1003
Oy 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerGluLeuGlnTyr 280
Dh 1004 ATGAGAAATCTCACTATGAAAGAGCTGACACAGTGGCTTCTCTGTAATTAACAATGC 1063
Oy 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyTyrPheGluGluMetLysTyr 300
Dh 1064 TTGAAAAGAGAGAGAGACAGTGAATCCATCGTGTATATTTGAAGAAATATAT 1123
Oy 301 LeuGluLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAla 320
Dh 1124 TTGGAACCTATGATGTTGTTAATGATCAACAAACGTATAAGAGAGATGCTTCTTCACGCA 1183
Oy 321 HisThrAsnAspPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGln 340
Dh 1184 CATACCAACACTTTGCCAAAGTCCGTCGTCACCTGTGATCTTATTTCAAGAGAACG 1243
Oy 341 LeuAsnThrArgValValLeuValAlaValGluThrThrPheGluLysAspGlnIleAsp 360
Dh 1244 CTCACACCAAGGCTTCTCTGTGGCTGTAGAACCTGGACTGAGAAAGGATCAGATTGAC 1303
Oy 361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIleLys 380
Dh 1304 ATCACCAACCAACCTGTGAGATGCTCATGATGTTCAAAATACCGGCGCCCATTAAG 1363
Oy 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSer 400
Dh 1364 CAGCATGCTGATGCTGTGACCTCATCTGCGGGTGCACATTTCAATAAGAACAGTAGT 1423
Oy 401 LeuSerTyrPheGlyGlyValLysSerArgThrArgGlyValGlyValAsnGluTyrGly 420
Dh 1424 CTGAGTACTTTTGGAGGTGTCTGTCTCCACAAAGAGAGTGTGTGATGAGTATGGT 1483
Oy 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440
Dh 1484 CTTCCCAATGGCAGTGCACAAATATTATCGCAGAGCTGGCTCAAAACCTTGGAAATCAA 1543
Oy 441 TrpGluProSerSerArgLysProLysCysAspCysThrGluSerTrpGlyLysIle 460
Dh 1544 TGGGAACCTTTTACGCAAGAACCAAAATGATGACTGCACAAATCCGCGGTGCTGCTGATC 1603
Oy 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr 480
Dh 1604 ATGGAGAAACAGAGGCTGCCATTTCTCGAAATTTTCAAGTGCACATTTTGGAAATAT 1663

Oy 481 ArgAspPheLeuGlnArgGlyGlyValAcLysLeuPheAsnArgProThrLysLeuPhe 500
Dh 1664 AGAGACTTTTACAGAGAGAGGTGGAGCTGCTCTTTTCAACAGGCCAACAAAGCTATTT 1723
Oy 501 GluProThrGluCysGlyAsnGlyTyrValGluAlaGlyGluGluCysAspCysGlyPhe 520
Dh 1724 GAGCCACGGAATGTGAAATGATGATGAGTGGAGCTGGGAGGAGTGTGATTTGGTTTTT 1783
Oy 521 HisValGluCysTyrGlyLeuCysLysLysCysSerLeuSerAsnGlyValHisCys 540
Dh 1784 CATGTGAATGCTATGATTAATGCTGAAGAAATGTTCCCTCCAAAGGGGCTCACAGC 1843
Oy 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGluCys 560
Dh 1844 AGCAGCGGGCTCTCTGTACAAATACCTCATGCTTTTTCAGCCACAGAGGTATGAAATGC 1903
Oy 561 ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCys 580
Dh 1904 CCGCATCTGTGAACGAGTGTGATTAATCAATATTTCTGAGACTGTGTCAGTGC 1963
Oy 581 ProProAsnLeuHisLysGlnAspGlyTyrTrpAlaCysAsnGlnAsnGlnLysArgCysTyr 600
Dh 1964 CCACCAATCTTCAATAAGCAAGACGATATGCAATGCAAAATCAGGGCCGTGCTTAC 2023
Oy 601 AsnGlyLysLysThrArgAspAsnGlnCysGlnTyrIleTyrGlyThrLysAlaAla 620
Dh 2024 AATGGCAGTGCAGACACAGACAGACAGTCTGATCAATCTGGGAAACAAAGCTGCA 2083
Oy 621 GlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGlyLysGlyAsnCys 640
Dh 2084 GGGCTGTACAAGTCTCTGTAAGAAAGCTGAATACAGAGGACATGAGAAAGGAAATGC 2143
Oy 641 GlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660
Dh 2144 GCGAAGATGAGACCGGTGATTCAGTGCAGCAAACTGATGTGTCTGTGATTCCTTA 2203
Oy 661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyGlnIleIlePro 680
Dh 2204 CTCTGTACCAATCTTACTCGAGCTCCACGTAATTTGTCACTTCAAGGGTGAATCATTTCCA 2263
Oy 681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValValLeuAsp 700
Dh 2264 ACTTCTTCTTACCACTCAAGGCGGGGTGATTCAGTGCAGTGTGCTTGTATGAT 2323
Oy 701 AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720
Dh 2324 GATGATACGGATGTGGCTATGTAGAAAGATGGAAGCCCATGTGGCCGTCTATGATGTCT 2383
Oy 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740
Dh 2384 TTACATGCGAAGTGCCTTAACAATTCAGGCCCTTAATATATGACACCTGTCCATGATTCC 2443
Oy 741 LysGlyLysValLysSerGlyHisGlyValLysSerAsnGluAlaThrCysIleCysAsp 760
Dh 2444 AAGGGTAAAGTCTTGGGGCATGGGGTGTGTGATATGAAGCACCACTTCGATTTGTGAT 2503
Oy 761 PheThrTrpAlaGlyTyrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780
Dh 2504 TTTCACCTGGCAGGAGACAGATTCAGATTCGGGATTCAGTTAGGAACCTTCACCCCTCC 2563
Oy 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
Dh 2564 AAGGATACAGAGACCAAGGGGCTCAGTGCACCAATCATTAATATAGCTCATGCTGCTGT 2623
Oy 801 AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTyrPheLysAsnValLys 820
Dh 2624 GCCATTCCTGTAGCAGCTATGTCTTGGGGGCACAGCTGGGATTTAAAAATGTCAAG 2683
Oy 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832
Dh 2684 AAGGAAAGTTCATCTTACTACCAAGGCCCATTC 2719

Db	2637	AGGAGCGGGCCCTGCTGTAAACAATACCTCATGCTTTTTCAGCCAGCAGGTAATGAATCC	2636
Qy	561	ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCys	580
Db	2697	CGGATACCTCTGAAACGAGTGTGATATTACTGAATATTGTACTGGAGACTCTGGTCACGTGC	2756
Qy	581	ProProAsnLeuHISLysGlnAspGlyTyrValaCysAsnGlnAsnGlnGlyArgCysTyr	600
Db	2757	CCACCAATCTTCTTAAGACAGACGAGATATGCAATCAATAATTCAGAGGGCGGTGGTAC	2816
Qy	601	AsnGlyLysCysLysThrArgAspAsnGlnCysGlnTyrIleTyrGlyThrLysAlaAla	620
Db	2817	AATGGCAGAGTGCAGACAGACAGACACAGATGTCAGTACATCTGGGGGAACAAAGCTCA	2876
Qy	621	GlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGluLysGlyAsnCys	640
Db	2877	GGGCTGTACAAAGTCTCTATGAAAAACCTGAAATACAAAGGCACTGGAAAGGAAATGC	2936
Qy	641	GlyLysAspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeu	660
Db	2937	GGGAAGAGATGGAGACCGGTGGATTCAATGCACGAAACATGATCTGTCTGGAGATTCTTA	2996
Qy	661	LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyGluIleLeuPro	680
Db	2997	CTCTGTACCAATCTTACTCGAGCTCCAGATGTAATGGTCAACTTCAGGGGTGAATCATTTCCA	3056
Qy	681	ThrSerPheTyrHisGlnArgValIleAspCysSerGlyAlaHisValLeuAsp	700
Db	3057	ACTCTCTCTTACCAATCAAGCCGGGTATTTAGCTGACGAGTGGTCCCATGTATGTTTAGAT	3116
Qy	701	AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetLeuCys	720
Db	3117	GATGATACGAGATGGGGCTATGTAGAAGATGGAAAGCCATGTCGGCCGTATGATGTGAT	3176
Qy	721	LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerCysProLeuAspSer	740
Db	3177	TTTAATATCGGAAGTCCCTPACAAATTCAGACCCCTTAATATGACACACCTGTCCACTGGATTCC	3236
Qy	741	LysGlyLysValCysSerGlyHisGlyValaCysSerAsnGluIaThrCysIleCysAsp	760
Db	3237	AAGGTTAAAGTCTGTTGGGGCCATGGGGGTGTGTAGTAAAGGCCACCTGCATTTGTGAT	3296
Qy	761	PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro	780
Db	3297	TTTCCACCTGGGCAAGGACAGATTGACAGTATCCGGGATCCAGATTAGAACCTTCACCCCCC	3356
Qy	781	LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly	800
Db	3357	AAGGATAGAGACCCCAAGGCTCTTAGTGCACCAATCTCATATAATAGGCTCATGGCTGGT	3416
Qy	801	AlaIleLeuValAlaAlaIleValaLeuGlyGlyThrGlyTrpGlyPheLysAsnValLys	820
Db	3417	GCCATCTCTGTAGACAGCTAATGTCTCTTGGGGGACAGAGCTGGGATTTAAAAATGTCACG	3476
Qy	821	LysArgArgPheAspProThrGlnGlnGlyProIle	832
Db	3477	AAGAGAGGTTGATCTTACTACACAGAGCCCATC	3512
RESULT 5			
US-10-144-771-15737			
: Sequence 15737, Application US/10144771			
: GENERAL INFORMATION:			
: APPLICANT: VENTER, J. Craig			
: TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF			
: FILE REFERENCE: C0001321			
: CURRENT APPLICATION NUMBER: US/10/144,771			
: CURRENT FILING DATE: 2002-05-15			
: NUMBER OF SEQ. ID NOS: 47235			
: SEQ. ID NO 15737			
: LENGTH: 2271			
: TYPE: DNA			
: ORGANISM: HUMAN			

US-10-144-771-15737			
Alignment Scores:			
Pred. No.:	9,65e-286	Length:	2271
Score:	3917.50	Matches:	714
Percent Similarity:	96.05%	Conservative:	16
Best Local Similarity:	93.95%	Mismatches:	25
Query Match:	86.04%	Indels:	5
DB:	9	Gaps:	2
US-09-634-252A-4 (1-832) x US-10-144-771-15737 (1-2271)			
OY	29	ProAlaGlySerValProAlaSerAlaProAlaArgThProProCysArgLeuLeu	48
Db	4	CCCCGCCGCCGGTG-----CCGGCCCCGGCGCCGCCCTGCTCTC	51
OY	49	ValLeuLeuLeuLeuProProLeuAlaAlaSerSerArgProArgAlaTrpGlyAlaIa	68
Db	52	GTCTTTCATCTCACTGACCTGCGCCGACCTCATCCGGCCCGCTCCGGGGCGCGCT	111
OY	69	AlaProSerAlaProHisTrpAsnGlyTrpAlaGlyLysAsnLeuGlyValLeuAlaAsp	88
Db	112	GGCCCGAGGCTCCGACTGGAATGAATGCGAGAAAAACCTGGGAGTCTGGAGAT	171
OY	89	GluAspAsnThrLeuGlnGlnAsnSerSerSer---AsnIleSerYSerAsnAlaMet	107
Db	172	GAAGACACACACTTGCACAAATAATAGCACAGAGAAATACAGACTACAGACATCGCAGTG	231
OY	108	GlnYsgIleThrLeuProSerArgLeuIleTyrTrpTlLeasnGlnAspSerGluSer	127
Db	232	CAAAAAGAAATACACTCGCTTCACACATGCGTGTATATCATCAACGAGCCTCAGAAAGC	291
OY	128	ProTyrHisValLeuAspThrLysAlaArgHisGlnGlyLysHisAsnLysAlaValHis	147
Db	292	CCCTATCATGTTCTTGACACAAAGGCCACACACACAAACACATAAAGCTGTGCAT	351
OY	148	LeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySerLysPheIleLeuAspLeuIle	167
Db	352	CTGGCCCAAGGCAAGCTTCCAGATCGAAAGCTTTCGGCTCCAAAGTTCATTCTTGACCTCAC	411
OY	168	LeuAsnAsnGlyLeuLeuSerSerAspTyrValGlnIleHisTyrGlnAsnGlyLysPro	187
Db	412	CTGAACAATGATGTTTGCTATCTTCTGACTACGTGAGAAATCCACTATGAAGAAGCGGAACAG	471
OY	188	GlnTyrSerLysGlyGlyGlnHisCysTyrTyrHisGlySerTlleArgGlyValLysAsp	207
Db	472	ATGTACTCTTAAGGTTGAGAGACACTGTACTACACGGAAGCATCAGAGCGTCAAGAT	531
OY	208	SerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAspTrpPhe	227
Db	532	TCCAGAGGTGGCTATACGACCTGCAGATGAGATCCAGATGCTTAAAGGTGACACCTTT	591
OY	228	ValTyrMetIleGlnProLeuGlnLeuValHisAspGlyLysSerThrGlyArgProHis	247
Db	592	GTGTATATGATGAGAGCTCTGGAACAGCTAGATGATGAGAAAAAGCAGGCCACACAC	651
OY	248	IleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMetGlu	267
Db	652	ATAATCCAGAAAAACCTTGGCAGACAGTATTCTTAACACATGAAGAATCTCACACAGAT	711
OY	268	ArgGlyAspGlnTrpProPheLeuSerGluLeuGlnTrpLeuLysArgArgLysArgAla	287
Db	712	GGCACTGACCACTGGCTTGTCTTACTCTGAATTAACAATGGCTGGAAGAAGAAAGAGCG	771
OY	288	ValAsnProSerArgGlyLlePheGlnGluMetLysTyrLeuGluIleuMetIleValAsn	307
Db	772	GTCAATCCATCTCGTGGTGTGTTTGAAGAAATGAATATTGGAGCTTATGATTGTTAAT	831
OY	308	AspHisLysThrTyrLysHisAspSerSerHisAlaHisThrAsnAspPheAlaLys	327
Db	832	GATCAACAAGACTATTAAGAAGACCGCTTCTTCACAGCCCATACCAACAACCTTGCAGAAAG	891
OY	328	SerValValAsnLeuValAspSerIleTyrLysGlnGlnLeuAsnThrArgValIleLeu	347


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Db      892 TCTGTGTCACACCTTGATGATTCTATTACAGAGAACGCTCAACACAGGCGGTGTCTG 951
      348 ValAlaValAlaGluThrTrpThrGluLysAspGlnIleAspIleThrThsAspProValGln 367
      952 GTGGCTGTGAGACCTGGACCGAGAGATCATCTGCATCATCACCATCAACCCCGTGGAG 1011
      368 MetLeuHisGluPheSerLysTyrArgGlnArgIleLysGlnHisAlaAspAlaValHis 387
      1012 ATGTCATACATGACTTCTCCACAGTACCGGCAATCAACAGACGCTGAGCGGTCCAC 1071
      388 LeuIleSerAlaValThrPheHisTyrLysArgSerSerIleuSerTyrPheGlyValAla 407
      1072 CTCATCTCGCGCGTACATTCCTCATTAAGAGAACACTGTGAGTTACTTTGGAGGCGTG 1131
      408 CysSerArgTrpGlnArgIleValAlaGlyValAlaGlnIleuProMetAlaValAlaGln 427
      1132 TGTCTTCGAATTAAGAGGGGTTGTGTGATGATGATGCTTCCAAATGGCGGTGGCACAA 1191
      428 ValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTrpGluProSerSerArgLys 447
      1192 GTATTATTCACAGAGCTGGCTCAAAACCTTGGAAATCCAGTGGGAACCTTCGAGCAGGAAG 1251
      448 ProLysCysAspCysThrGluSerTrpGlyLysIleMetGluGluThrGlyValSer 467
      1252 CCAAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1311
      468 HisSerArgLysPheSerLysCysSerIleLeuGluTyrArgAspPheLeuGlnArgGly 487
      1312 CACTCTCGAAAGTCTCAAAAGTCAGACATTTGGAGTACAGACATTTTACAGAGAGCT 1371
      488 GlyGlyAlaCysLeuPheAsnArgProThrLysLeuPheGluProThrLysCysGlyAsn 507
      1372 GCGGAGAGATGCTTTTCAATAGCCCACTAAGCTGTGTGAGCCCAAGGAAATGTGAAAT 1431
      508 GlyTyrValAlaGluAlaGlyLysCysAspCysGlyPheHisValAlaGlyLysGlyLeu 527
      1432 GGATATGTGAGAGCGCGGAGGAGATGCGACTGTGGTTCCATGTGGAATGCTATGAGATT 1491
      528 CysCysLysLysCysSerLeuSerAsnGlnAlaHisCysSerAspGlyProCysCysAsn 547
      1492 TGTCTGTAAGAAAGTGTCTGCTTCCAAATGGGCGCCACTGACAGTACCGCCCTGTCTAAC 1551
      548 AsnThrSerCysLeuPheGlnProArgGlyTyrGluLysArgAspAlaValAlaGlnLys 567
      1552 AACACCTCATGCTTTTTCAGTCACGAGGATGAAATGTGCGGATCCCTTAACACTGCT 1611
      568 AspIleThrGluTyrCysThrGlyAspSerGlyLysCysProProAsnLeuHisLysGln 587
      1612 GATATTCACCGAGATCGCACTGGAGACTGTGGCCACTGCCACGGAACCTCCATAACAA 1671
      588 AspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyrAsnGlyLysLysThrArg 607
      1672 GATGGCTATAGCTGCATATAAATCAGGGCTGCTTACAAATGGCAGTGCAGAGCAAGG 1731
      608 AspAsnGlnCysGlnTyrIleThrPglTyrLysAlaAlaGlySerAspLysPheCysTyr 627
      1732 GACAATCATTCGACATCTGCGGAGCAAAAGCTGCGGGGTCAGAGCAAGTCTGTGTAT 1791
      628 GluLysLeuAsnThrGluGlyThrGluLysGlyAsnCysGlyLysAspGlyAspArgTyr 647
      1792 GAAAGCTGATACACGAGAGAGCAGCAGGAAAGGCAATGTGGAAAGGTGAGAGCCGCTGG 1851
      648 IleGlnCysSerLysHisAspValPheCysGlyPheLeuLeuSerTyrTrpAsnLeuThrArg 667
      1852 ATCCCGTGCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1911
      668 AlaProArgIleGlyLysLeuGlnGlyLysIleIleProThrSerPheTyrHisGlnGly 687
      1912 GCTCCACGATATGCTGATCACTTCAAGAGAGATCATCCGACTCTCTTATCATCAAGGC 1971
      688 ArgValIleAspCysSerGlyAlaHisValAlaLeuAspAspAspThrAspValGlyTyr 707

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Db      1972 CGAGTATTGACTGCAGTGGTCTCATGTAGTTTACAGCATGATACAGACGTGGGTTAC 2031
      708 ValGluAspGlyThrProCysGlyProSerMetCysLeuAspArgLysCysLeuGln 727
      2032 GTTGAAGATGGGACCTCCGCTGTGGCCCTCCAGATGATGCTTGAAGTGGAGAGGCTTAAG 2091
      728 IleGlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGlyValAlaCysSerGly 747
      2092 ATTCAAGCCCTGAATATGACAGCTGCCACTTGTACTCAAGGGATTAAGTCTGCTCCGCG 2151
      748 HisGlyValCysSerAsnGlnAlaThrCysIleCysAspPheThrTrpAlaGlyThrAsp 767
      2152 CACGGGGTGTGTAGACAGCAAGACCCACTGATCTGTGATTTCACTGGGACAGCAGAC 2211
      768 CysSerIleArgAspProValArgAsnLeuHisProPolysAspGlnGlyProLysGly 787
      2212 TCCACATCCGGGATTCACATTTGGAAACCCCAACCCCTTAAGATGAAGGCCCTTAAGGT 2271

RESULT 6
US-09-949-016-5332
; Sequence 5332, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5332
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5332

Alignment Scores:
Pred. No.: 5,1e-273 Length: 2394
Score: 3749.50 Matches: 684
Percent Similarity: 99.27% Conservative: 0
Best Local Similarity: 99.27% Mismatches: 1
Query Match: 82.35% Indels: 4
DB: Gaps: 1

US-09-634-252A-4 (1-832) x US-09-949-016-5332 (1-2394)
      145 AlAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySerLysPheIleLeu 164
      5 GCTGTTCATCTGGCCCGCAGCAGCTTCAGATTGAACCTTCGCGCTCCAAATTCATTCTT 64
      165 AspLeu-IleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIleHisTyrGluAs 184
      65 GACCTCATAT-----GGTTGTGTCTCTCGATTATGTGAGATTCACCTAAGCAAAA 115
      184 nGlyLysPProGlnTyrSerLysGlyGlyLysHisCysTyrTyrHisGlySerIleArgI 204
      116 TGGGAAACACAGTACCTTAAGGTGAGAGCACTGTACTACCATGGAAGCATCAGAGG 175
      204 yValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGluAs 224
      176 CGCTAAAGACTCCAGAGTGGCTCTGTCAACCTGCAATGCAATGCAATGCTTTGAAGA 235
      224 pAspThrPheValTyrMetIleGluProLeuGluLeuValHisAspGluLysSerThrG 244
      236 TGATACCTTGCTGTATATGATAGAGCCACTAGACCTGCTTCAATGATGAGAAACACAGG 295
      244 yArgProHisIleIleGlnLysThrLeuAlaGlyLysTyrSerLysGlnMetLysAsnLe 264

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Db      |||
296 TCACACACATATATATCCAGAAACCTTGGCAGACAGTATTCTAACCAATGAAGATCT 355
Qy      |||
264 UTHrMetGLuArgGLyAspGLnTrpProPheLeuSerGLuLeuGlnTrpLeuLysArg 284
Db      |||
356 CACTATGGAAGAGGTGACAGGAGGCGCTTCTCTCTGAAATTAACAGGGTGAAGAAAG 415
Qy      |||
284 gLysArgAlaValAsnProSerArgGLyLeuPheGLuLeuMetLysTrpLeuGluLys 304
Db      |||
416 GAAGAGAGGAGTGAATCCATCAGCTGGTATATTGAAGAAATGAATATTGGACACTTA 475
Qy      |||
304 LLeuValAsnAspHisLysThrTrpLysLysHisArgSerSerHisAlaHisThrAsn 324
Db      |||
476 GATTGTTAATGATCACAACCAATGAAGACATCGCTCTTCATCATCAGATCAACA 535
Qy      |||
324 nPheAlaLysSerValValAsnLeuValAspSerLLeuTrpLysGLuGlnLeuAsnTrp 344
Db      |||
536 CTTTGCAAAAGTCCGGGTGCAACCTTGAGTCTATTACAGAGAGCGCTCAACAACAG 595
Qy      |||
344 gValValLeuValAlaValGLuTrpTrpTrpGLuLysAspGLnLeuAspLLeuThrAs 364
Db      |||
596 GGTTCCTGCGTGGCTGAGAGACCTGGACTGAGAAAGATCAGATTGACATCCACCA 655
Qy      |||
364 nProValGlnMetLeuHisGLuPheSerLysTrpArgGLnArgLLeuLysGlnHisAla 384
Db      |||
656 CCTGTGCAGATGCTCCATGAGTCTCAAAATACCGGACGCGCATTAAGCAGCATG 715
Qy      |||
384 pAlaValHisLeuLLeuSerArgValThrPheHisLysTrpArgSerSerLeuSerTrp 404
Db      |||
716 TGTGTGCACCTATCTCCGGGTGACATTTCACTATTAAGAGAGCGTGTGAGTACT 775
Qy      |||
404 eGLyGLyValCysSerArgThrArgGLyValGLyValAsnGLuTrpGLyLeuProMet 424
Db      |||
776 TGGAGGTGCTGCTTTCGCGACAGAGAGTGGTGAATGAGATGCTTCCAAATGCG 835
Qy      |||
424 eValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGLyLLeuLTrpGLuPro 444
Db      |||
836 AGTGGACAAAGTATTTATCGCAGAGCGCTGCAAAACCTTGGAATCCAAAGGGAAC 895
Qy      |||
444 rSerArgLysProLysCysAspCysTrpThrGlnSerTrpGLyCysLLeuMetGLu 464
Db      |||
896 TACACAAAGCCCAAAATGTCAGCTGACAGCAATCTGGGGTGGCTGCAATGAGGGA 955
Qy      |||
464 rGLyValSerHisSerArgLysPheSerLysCysSerLLeuGlnLTrpArgAspPhe 484
Db      |||
956 AGGGGTGCTCCATTTCTGAAATTTTCAAGTGCAGATTTTGGAGATATAGAGACT 1015
Qy      |||
484 uGlnAlaArgGLyGLyAlaCysLeuPheAsnArgProThrLysLeuPheGLuProThr 504
Db      |||
1016 ACAGAGAGAGGAGGAGCGCTGCTTTTCAACAGCGCCCAAAACCTATTGAGCCAC 1075
Qy      |||
504 uCysGLyAsnGLyTrpValGLuLLeuLLeuGLuGLuLysAspCysGLyPheHisVal 524
Db      |||
1076 ATCTGGAATATGCTGACTGGAACCTGGGAGAGTGTGATTTGTTTATGTTGGAAT 1135
Qy      |||
524 sTrpGLyLeuCysCysLysLysCysSerLeuSerAsnGLyAlaHisCysSerAsp 544
Db      |||
1136 CTATGATATATGCTGTAAGAAATGTTCCCTCCACAGGGGCTACATGCGAGCGGCC 1195
Qy      |||
544 oCysCysAsnAsnTrpSerCysLeuPheGlnProArgGLyTrpGLuCysArgAspAla 564
Db      |||
1196 CTGCTGTAAACAATCACTCATGCTTTTTCAGCCACAGGGTATGAAGCGGGATGCT 1255
Qy      |||
564 LAsnGLyCysAspLLeuThrGLuTrpCysTrpArgLysSerGLnGlnCysProProAsn 584
Db      |||
1256 GAACGAGTGTGATATACGAAATATGTACTGAGAGCTCTGTCAGTCCAGCCACCA 1315
Qy      |||
584 uHisLysGlnAspGLyTrpAlaCysAsnGlnAsnGLnGLyArgCysTrpArgAsnGLy 604
Db      |||
1316 TCATTAAGCAAGAGGAGTATGCAATCAATCAAGGCGCGCTGCTACAAATGCGCG 1375
Qy      |||
604 sLysTrpArgAspAsnGlnCysGlnTrpLLeuTrpGLyThrLysAlaLLeuLysAsp 624

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Db      |||
1376 CAAGACCAGAGACCAACGAGTGTCTAGTACTGGGGAAACAAAGCGCTGAGCTGACAA 1435
Qy      |||
624 sPheCysTrpGLuLysLeuAsnTrpGlnGLyThrGlnLysGLyAsnCysGLyAspGL 644
Db      |||
1436 GTTCTGCTATGAAAGCTGGAATACAGAGAGGAGCTGAGAGGGAACCTGCGGAGAG 1495
Qy      |||
644 yAspArgTrpLLeuGlnCysSerLysHisAspValPheCysGLyPheLeuLeuCysThr 664
Db      |||
1496 AGACGGGGAGTTCAGTGCACCAAAACATGATGTGTGCTGGATTTCTTACTGTACCA 1555
Qy      |||
664 nLeuThrArgAlaProArgLLeuGLyGlnLeuGlnGLyLLeuLLeuProThrSerPhe 684
Db      |||
1556 TCTTACTGAGCTCCAGCTATGTTGTCAACTTCAGAGGTGAGATCAATTCCAACTTC 1615
Qy      |||
684 rHisGlnGLyValGlnLLeuAspCysSerGLyAlaHisValValLeuAspAspTrp 704
Db      |||
1616 CCATCAAGCGCGGTGATGACTGCTCAGGAGGAGCCCATGATGTTTAAATGATGAT 1675
Qy      |||
704 pValGLyTrpValAluAspGLyTrpProCysGLyProSerMetMetCysLeuAspArg 724
Db      |||
1676 TGTGGCTATGTAGAAAGTGAAGAGCGCATGTGGCCGCTGTGATGTTTAAATCGGAA 1735
Qy      |||
724 sCysLeuGlnLLeuAlaLeuAsnMetSerSerCysProLeuAspSerLysGLyLys 744
Db      |||
1736 GTCCCTACAAATTCAGCCCTAAATATGAGCAGCGCTGTCACCTGATTCAGAGGTA 1795
Qy      |||
744 LcysSerGLyHisGLyValCysSerAsnGLuAlaThrCysLLeuCysAspPheTrp 764
Db      |||
1796 CTGTTCGGGCGCATGGGTGTGTAGTAAGAGCCAGCTGCAATTTGTGTACCTGGGC 1855
Qy      |||
764 aGLyTrpAspCysSerLLeuArgAspProValArgAsnLeuHisPropLysAspGL 784
Db      |||
1856 AGGAGACAGATGTGAGTATCCGGATCCAGTTAGAGAACCTTCAACCCCAAGAGTA 1915
Qy      |||
784 yProLysGLyProSerAlaThrAsnLeuLLeuLLeuSerLLeuAlaGLyAlaLLeu 804
Db      |||
1916 ACCCAAGGCTCTGATGCGCACCAATCTCATATAGCGCTCCATGCTGCTGCTGCT 1975
Qy      |||
804 LAlaAlaLLeuValLeuGlnGLyTrpTrpGLyTrpGLyPheLysAsnValLysAsp 824
Db      |||
1976 AGCAGCTATTTGCTTGGGGGACAGAGCTGGGGATTTAAATAATGCAAGAGAGAG 2035
Qy      |||
824 eAspProThrGlnGlnGLyProLLeu 832
Db      |||
2036 CGATCCTACTACAGCAAGGCCCATC 2060

RESULT 7
US-10-144-771-3346
: Sequence 3346, Application US/10144771
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig
: TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
: FILE REFERENCE: CLO01321
: CURRENT APPLICATION NUMBER: US/10/144, 771
: CURRENT FILING DATE: 2002-05-15
: NUMBER OF SEQ ID NOS: 47235
: SEQ ID NO 3346
: LENGTH: 3231
: TYPE: DNA
: ORGANISM: HUMAN
: US-10-144-771-3346

Alignment Scores:
Pred. No.: 2,01e-141 Length: 3231
Score: 2010.00 Matches: 405
Percent Similarity: 62.00% Conservative: 91
Best Local Similarity: 50.62% Mismatches: 230
Query Match: 44.15% Indels: 74
DB: Gaps: 19

US-09-634-252a-4 (1-832) x US-10-144-771-3346 (1-3231)
Qy      47 LeuLeuValLeuLeuLeuProProLeuAlaLLeuSerSerArgProArgAlaTrpGLy 66

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Db      40 ATCGGGCTGCTGCTGTTACCGCTTCC-----CCGGCCGGCTTTGG 87
Oy      67 AAlaAlaPro---SerAlaProHisTrpAsnGluThrAlaGluLysAsnLeuGlyVal 85
Db      88 GCCCTGGGTCCCGAGAGAGCTCTGCACGTGAGAGAGCTCAGCC-----CATGTGGGG--- 138
Oy      86 LeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsnIleSerTyrSerAsn 105
Db      139 -----AGCCCGAGAGCT 150
Oy      106 AlameGlnLysGluIleThrLeuProSerArgLeuIleTyrThrIleAsnGlnAspSer 125
Db      151 CCAGAGGCTCTAGGTCACAGAGCCAGCCGCTGTAGAGCAG---ACCTCCGGGGGA 207
Oy      126 GluSerProTyrHisValLeuAspThrIleArgHisGlnGlnIleLysHisAsnLysAla 145
Db      208 GAGCTCCGAAGACAGTGGAGACACAGGCTCCCGCAGAGTCCGCCAGAGGGGAGCCCT 267
Oy      146 ValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySerLysPheIleLeuAsp 165
Db      268 GTTCACCTGGCCCGAGGTGAGTTCGTATCCCGCCCTTCGACTCAACCTTCACCTGGAC 327
Oy      166 LeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIleHisTyr---GluAsn 184
Db      328 CTGAGCTGACATCATCCTCTCTCTCTCCAGATGTGAGAGCCGACCTTCACCGGAG 387
Oy      185 GlyLysProGlnTyrSerLysGly---GlyGlnHisCysTyrTyrHisGlySerIleArg 203
Db      388 GGAACAAGACACACAGCAGCTGGGGCTGAGACACAGCTACTACCTAGGGAACCTCCG 447
Oy      204 GlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGlu 223
Db      448 GGCACCCACAGCTCTTCTGCTGCACTCTACATGCCAGGGGCTGCATGGGGCTTCTCT 507
Oy      224 AspAspThrPheValTyrMetIleGluProLeuGlnLeuVal-----HisAspGluLys 241
Db      508 GATGGCAACTGACTTACATCATGAGACCTAAGAGATAGTACGCGCCCTGGGGACCCCA 567
Oy      242 SerThrGlyArgProHisIleIleGlnLysThr----- 252
Db      568 CAGGAGCCCTTCCGCCATTTACCGGAGCCCTCTCTCCAGCCCTTGATGC 627
Oy      253 -----LeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMet 266
Db      628 AGGAGCCAGGCTCCCTGTTGCTGCTCCGCCAGCTGCTCTCCCAAC----- 678
Oy      267 GluArgGlyAspGlnTrpProPheLeuSerGluLeuGlnTrpLeuLysArgArgLysArg 286
Db      679 -----TGCCCAAGCTA-----AGAAAGAAAGG 702
Oy      287 AlaValAsnProSerArgGly-----IlePheGluGlnMetLysTyrLeuGlnLeu 303
Db      703 CAGGTCCGC-----AGGGGCCACCCACAGTGCACAGCGAGCAAGTATGTGAGTTG 756
Oy      304 MetIleValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAlaHisThrAsn 323
Db      757 ATTGTATTCATGACCCACAGCTGTTGAGAGATGGGAGAGTGAAGTGTCTACACAGC 816
Oy      324 AsnPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGlnGlnLeuAsnThr 343
Db      817 AACTTTGCAAAATCTGTTGAACTGGACGTGATATACAGAGAACAGCTCAACACA 876
Oy      344 ArgValValLeuValAlaValGluThrTrpThrGluLysAspGlnIleAspIleThrThr 363
Db      877 AGAATTTCTGTGTGGCATGGAACGTGGCAGATGGGACAGATCCAGTGCACAGAT 936
Oy      364 AsnProValGlnMetLeuHisGluPheSerLysTyrArgLysArg---IleLysGlnHis 382
Db      937 GACCTACTGAGACCTCGCCGGCTTATGTCTACCGCGGAGAGGTCTCCCTGACGCC 996
Oy      383 AlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSerLeuSer 402
:::||||| ||||| ||| |||||

Db      997 AGTATGCCACCCACCTCTTCTCGGTTAGACCTTCCAAAGACACAGCGGGGGCGCC 1056
Oy      403 TyrPheGlyGlyValCysSerArgThrArgGlyValGlyValAsnGluTyrGlyLeuPro 422
Db      1057 TAGCTGGAGGAGCTGTGTTACACTGTCCAGGGGAGGTGTGTACACAGATGTAACAATC 1116
Oy      423 MetAlaValAlaGlnValLeuSerGlnSerIleuAlaGlnAsnLeuGlyIleGlnTrp--- 441
Db      1117 GGTCCATGGGCGTGAACCTGGGCCAGAGCTTAGGCGAACAACCTTGGCGATGATGGAAAT 1176
Oy      442 GluProSerSerArgLysProLysCysAspCysThrGluSerTrpGlyCysIleMet 461
Db      1177 AACCAACCGAGCTCAGACAGGGGAGCTCAGATGTCCAGACATTTGGCTGGGCTGATCARG 1236
Oy      462 GluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyrArg 481
Db      1237 GAGGACATGGGTTCATTTGCCCCCAAGTTTCGCGTGCAGATCCAGCAATTAACAAC.1296
Oy      482 AspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsnArgProThrLysLeuPheGlu 501
Db      1297 CAGTTTCTGAGAGAGGAGGAGGAGCTGCTTTCACAGCCCTCAAGCTTTCGAGC 1356
Oy      502 ProThrGluCysGlyAsnGlyTyrValGluAlaGlyLeuGluCysAspCysGlyPheHis 521
Db      1357 CTTCCGAGAGTCCGAAACGGCTTCGTGAGGCGGAGAGAGTGCAGACTGCGGCTGCTG 1416
Oy      522 ValGluCysTyr-----GlyLeuCysCysLysLysCysSerLeuSerAsnGlyAla 538
Db      1417 CAGGAGTGCAGCCGACGAGGAGGCAACTGCTGTAACAAATGACCTTGACGACGACGCC 1476
Oy      539 HisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyr 558
Db      1477 ATGTGCAGCATGGCTCTTGTCTGCCGC-----TGCAAGTATAGGCACAGAGTGTTC 1530
Oy      559 GluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGly 578
Db      1531 TCTTCCGGAAGACCGGTGAATGAGTGCATTCGAGAGACCTGCACACCGCGCTCAACG 1590
Oy      579 GlnCysProProAsnLeuHisLysGlnAspGlyTyrValAlaCysAsnGlnAsnGlnGlyArg 598
Db      1591 CAGTGTCCCTTAACCTTCAACAGCTGACGAGCTTACTGATATCATGACGAGGTCTGT 1650
Oy      599 CysTyrAsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleTrpGlyThrLys 618
Db      1651 TCGTATGAGAGCGCGCTGTAACCCGGAGCCGAGCAGTGAACCCATGAGGCGCATGCG 1710
Oy      619 AlaAlaGlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlnTrpLysGly 638
Db      1711 GCTGCG-----GATCGTTCTGTATGAGAACCTGAACGTGAGGAGGACAGAGCTGGA 1764
Oy      639 AsnCysGlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPheCysGly 658
Db      1765 AACTGTGAGCGCAAGGATGTGTTGGGTCCAGTGCAGTAAACAGATATGCTGTGCGC 1824
Oy      659 PheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyIle 678
Db      1825 TTCTCTTGAGCGTCACATCTCTGAGAGTCCCGGCTAGGAGATGTGGGGGCGACATC 1884
Oy      679 IleProThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValAla 698
Db      1885 AGCAGTGTCACTTTCACACAGGCGCAAGAGTGGACGTGCAGAGGAGGCGCACGTGCAG 1944
Oy      699 LeuAspAspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMet 718
Db      1945 CTAGCTATGGCTGAGACCTGAGTATGTGAGAGCAGCGCACGGCTGTGGGCCAACATG 2004
Oy      719 MetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerCysProLeu 728
Db      2005 TTGTGCTAGTACCCCTCGCTCCAGCTCTGCTTCAACCTTCAACACCTCGCCCTGGA 2064
Oy      739 AspSerLysGlyLysValLysSerGlyHisGlyValLysSerAsnGluAlaThrCysIle 758
Db      2065 ACTGAGAGCGAAGAGTCTCTCCATCATGTGGGTTTGACAGCAAGAGGGAAGTGTATC 2124
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Oy      Cysapghethrrtpalaglythrapsycyserllelrqspvrolatgashleuhls 778
Db      2125 TGTACGCCAGACTGTCAGCAGCAAAAGACTGCATTTTACAACCCTCCAGCGTGCT 2184
Oy      779 ProPro---LysaspGIUGlYProLySGIYProSerAlathrasneullelgLYser 797
Db      2185 CCCACTGGGAGAGACTGACATACAAAAGGTCGCCAGCGCTCACCATCATCATTTGGATTCC 2244
Oy      798 llaalaiaalleuevalaleaalaeleualenuglylthrgltyrpglyPhyllys 817
Db      2245 ATCGCCGGGGCTGTCTGTCGCGACCATGCTCTGGCGCGGCGCATGGAATTTAAG 2304

RESULT 8
US-10-170-235-7480
Sequence 7480, Application US/10170235
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craly
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 7480
LENGTH: 2875
TYPE: DNA
ORGANISM: HUMAN
US-10-170-235-7480
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Alignment Scores:	
Pred. No.:	2,77e-140
Score:	1994.00
Percent Similarity:	59.64%
Best Local Similarity:	45.95%
Query Match:	43.80%
DB:	8
Length:	2875
Matches:	403
Conservative:	120
Mismatches:	253
Indels:	102
Gaps:	19

QY 1 MetuysproProGlySerSerSerArgAlaProProLeuAla-----Gly 15
 Db 12 CTCGCCCGGCGACGGAGCGTCCGGCAACACACATACACACTGAGCCCGCGGAGGT 71
 QY 16 CysSerLeu-----AlaGlyAlaSerCysGlyProGlnArgGlyPro 29
 Db 72 TGCAGCCGCCACGGCGCGCGCAGCACCGCGCGGGCTGGTGGAGGTGGCGGGAGGCC 131
 QY 30 AlaGly-----SerValProAlaSerAlaProAla----- 39
 Db 132 CGGGGGCGCGGACCGAGGGAACCGACTCGGCGCGCGGCGGACATGAGAGCTGACCGTCTC 191
 QY 40 -----ArgThrProProCysArgLeuLeuLeuValLeuLeuLeuLeuPro 54
 Db 192 GGGCGAGCGCGGCTGACGCGCAGCACCATCGCAGG----- 224
 QY 55 ProLeuAlaAlaSerSerArgProArgAlaTyrGlyAlaAlaAlaProSer-----Ala 72
 Db 225 -----CGGCAGTGGTGTTGTCCTGCCCTTCTTGTCTGCTG-TTC 260
 QY 73 ProHisTTrpAsnGluThrAlaGluCylsAsnLeuGluValLeuAlaAspGluAspAsnThr 92
 Db 261 GTGTCTCGGAGACCTGCGCTCCGGCGGC-TGGCGGCGAGCAGGAGCGGCTCATTTATG 319
 QY 93 LeuGlnGlnAsnSerSerSerAsnGlnLeuSerTyrSerAsnAlaMetGlnGlyGluIleThr 112
 Db 320 GAGCTACAGAGAGAGAGAAAC-----CGCTTCGTGGAGCGCCACAG-ATC 367
 QY 113 LeuProSerArgLeuIleTyrTyrIleAsnGlnAspSerLeuSerProTyrGlnIleValLeu 132
 Db 368 GTGCCACATGGCGCTCATCTACCGCTCGGGGGCGAGACAGCAAACTCGGCACAGCGCTTC 427
 QY 133 AspThrTyrAlaArgHisGlnGlnIleLysHisAsnLysAlaValHisLeuAlaGlnAlaSer 152

Db	428	GACAGCGGGTGGCGGGGACCTCGGTGGCCGGACGTTGACATCTTTGACCAAGCAAC	487
Oy	153	PheGlnIleGluAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGlyLeu	172
Db	488	TTCCAGGTGATGCTCTTGGACGTCATTCATTTCTCGATGCTGCTAAATCATGATTTGG	547
Oy	173	LeuSerSerAspTyrValGluIleHisTyrGluAsn---GlyLysProIleTyrSerLys	191
Db	548	CTGTCTCTGTATATCATATGAGAGACACATTGACATGAGCAAGCATCTGGACGTTAA	607
Oy	192	GlyGlyGlnHisCysTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAla	211
Db	608	GGAGAGAGACACTGTTACTACCAAGGCCATATCCGAGAAACCTGACATTCATTTGTTGA	667
Oy	212	LeuSerThrCysAsnGlyLeuHisIleGlyMetPheGluAspThrPheValTyrMetIle	231
Db	668	TTTGTCACATGCCACAGCACTTCATGGAGTTTCTATGAGGGAGAACACACATATTCATTT	727
Oy	232	GluProLeuGluLeuValHisAspGluLysSerThrGlyArgPro-----His	247
Db	728	GAGCCA-----GAGCAAAATGACACTACTCAAGAGATTTCCATTTTCAT	772
Oy	248	IleIleGlnLysThrLeuAlaGlyIleTyrSerLys-----Gln	260
Db	773	TCAGTTTCAAAATCCAGACACTGTTTGAATTTTCCCTGGATGATCTTCCATCTGAATTTTCAG	832
Oy	261	MetLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerGluLeuGlnTyr	280
Db	833	CAAGTAAACATTTACTCATCAAAA-----TTTATTTTGAACCCAGACCA	877
Oy	281	LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlnGluMetLysTyr	300
Db	878	AAAGAGAGTAAACGGCACCTTCGTGATCTCTCGTAATGTGAAGAAAGAAACCAATATAC	937
Oy	301	LeuGluLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerHisAla	320
Db	938	ATTGACACTGATGATGTGATGATCATCACCTTATGTTTAAAAAATCGCGCTTCCGTTGA	997
Oy	321	HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGluGln	340
Db	998	CATACCAATACCTTATCGCAATCTGTGGGAACATGGCCAGATTATATATAAGACCA	105
Oy	341	LeuAsnThrArgValValLeuValAlaValGluThrTyrThrGluLysAspGlnIleAsp	360
Db	1058	CTTAAAGACACAGATGTATGCTGCTCTATGAAACCTGGCGACATGCACAAATGTTGCC	111
Oy	361	IleThrThrAsnProValGlnMetLeuHisGlnPheSerLysTyrArgGlnTyr---Ile	379
Db	1118	ATATCTGAAATCCATTGATCATCCCTACCTGATGAGTTATATGAATATACAGAGGGATTTATAC	117
Oy	380	LysGlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSer	399
Db	1178	AAAGAGAAAGATGATGCACTTCACCTTTTTCGGGAAGTCATATTCAGCATGACCGGAGC	123
Oy	400	SerLeuSerTyrPheGlyGlyValLysSerArgThrArgGlyValGlyValAsnGlyTyr	419
Db	1238	GGGCGACGCTTATATTGGTGGGATTTGCTCGTTGCTGAAAGGAGAGGCGCTGATGTAATTT	129
Oy	420	GlyLeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIle	439
Db	1298	GGGAAAACTGATTAATGCGCTGTTACACTTGGCCAGTCATTCAGCCCATTAATATTTGGTATTT	135
Oy	440	GlnThrGluProSerSerArgLysProLys-----CysAspCysThrGlu	454
Db	1358	-----ATCTCAGACAAAGAAAGATTAGCAAGTGTGAATGTAAATTCGAGGAC	1400
Oy	455	SerThrGlyGlyCysIleMetGluIleThrGlyValSerHisSerArgLysPheSerLys	474
Db	1406	ACGTGTGCTCGGGTGTATATGGGAACACACTGGCTATATCTTCCTTAATAAGTTTACCCAG	1466
Oy	475	CysSerIleLeuGluTyrArgAspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsn	494


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Db      668  TTGTCACATGCCAGCAGCTTCATGATGACGGAGAACACATATCTCATT 727
Oy      232  GLUPROLEUGLULEVALHISAPGLUYSSERTHGLYARGPRO-----HIS 247
Db      728  GAGCCA-----GAGAGAAATGACACTACTCAAGAGAGATTCCATTTCAT 772
Oy      248  ILEILEGLUYTHLEUALAGLYGINTYRSERLYS-----Gln 260
Db      773  TCAGTTTCAAAATCCAGACTGTTTGAATTTCTTGATGATCTTCATCTCAATTTCAG 832
Oy      261  METLYSASNLEUTHMETCULARGGLYSPGLINTYRPPROPHLEUSERGLULEGINTYR 280
Db      833  CAAGTAAACATTACTCCATCAAAA-----TTTATTTTGAAGCCAAAGACCA 877
Oy      281  LEUYSARGARGLYARGALALVALASNPROSERARGGLYILEPHLEGLULUMELTYR 300
Db      878  AAAAGGAGCTAAACGGCAGCTTCGCGATATCTCTGTAATGTAGAACAGAACAAATAC 937
Oy      301  LEUGLULEUMELLEVALASNAPHSISLYSTHYRGLYSLYSHISARGSERHISALE 320
Db      938  ATTGAACGATGATGTGATGATGATCACCCTTATGTTAAACATCGCGCTTCGGTGA 997
Oy      321  HISTHRASNAPHEALALYSSERYALVALASNLEUVALASPSERILETYRGLYGLIN 340
Db      998  CATACCAATACCTATGCGAAATCTGTGCGAACATGCGAGATTTATATATAAGACAN 1057
Oy      341  LEUASNTPRARGVALVALLEUVALALVALIGLINTHTRPHGLULYSPGLINILEASP 360
Db      1058  CTTAAGACGAGATGATGTGCTTATGCTTATGGAACCTGGCGACATGACAAAGTTTGC 1117
Oy      361  ILETHRTRASNPROVALGLINMETLEUNHISGLUPHESERYTYRARGGLINARG---ILE 379
Db      1118  ATATCTGAANAATCCATGTGATCCCTACCTGAGTTTATGAATACAGGAGGATTTATC 1177
Oy      380  LYSGLINHISALASPALVALHISLEUILESERARGVALTHRPHENISTYRYSARGSEC 399
Db      1178  AAAGGAGAAAGTAGAGCAGATTCACCTTTTTCGGGAGATCAATTTAGAGATACCCGAG 1237
Oy      400  SERLEUSERTYRPHGLYGLYVALCYSSERARGTHARGGLYVALGLYVALASNGLUYR 419
Db      1238  GGGCAGCGCTTATATGTTGGGATGTTGCTGCTGCTGAAAGAGAGAGCGCTGAATGAT 1297
Oy      420  GLYLEUPROMELALVALALAGLVALLEUSERGLINSERLAALAGLNASLEUGLYILE 439
Db      1298  GGGAAATGATTAATGAGCTGTACACTTGCACAGTCATTAGCCCATATATATGCTATT 1357
Oy      440  GLINTPRGLUPROSERSERARGLYSPROLYS-----CYSAPCYSTHARGLU 454
Db      1358  -----ATCTCAGACAAAGAAAGATTAGCAAGTGTGAATGTAATCCGAGGAC 1405
Oy      455  SEETPRGLYGLYCYSLIEMERGILUGLINTHARGLYVALSERHISERARGLYSPHESER 474
Db      1406  ACGTGCTCGGGTGATATATGGAGACACCTGGCTATATCTTCCTTAAAGTTCCACCCAG 1465
Oy      475  CYSSERLILEUGLUTYRARGSPHELEUGLINARGGLYGLYGLYVALCYSSLEUPHEASN 494
Db      1466  TGTATATATTGAAGACTATCATCTCCGATAGTGGAGAGTGTCCTCCGCTTTTCAAC 1525
Oy      495  ARGPROTHIRLYSLEUPHLEGLUPROTHRGILUCYSGLYASNGLYTYRVALGLUALAG 514
Db      1526  AAACCTCTAAGCTCTTGATCTCTCTGAGTGTGCAATAGGCTTCATGAAGCTGAGAG 1585
Oy      515  GLUCYASPCYSGLYPHENISVALGLUCYSTYR-----GLYENUCYSLYSLYS 531
Db      1586  GAGGTGTGATTGTGGAACCCGGCGCGAATGTGCTTGAAGAAGACAGAGTGTGTGAAGAA 1645
Oy      532  CYSSERLIEUSERASNGLYALAHISCYSSERASPGLYPROCYCYSASNANSTHRSER 551
Db      1646  TGCACCTTGACAGACTCTCAATGACAGTGCAGGCTTTGCTGTAA-----AAGTGC 1699
Oy      552  LEUPHEGLINTPRARGGLYTYRGLUCYSGARGSPALVALASNGLUCYASPILETARGLU 571

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Db      1700  AAGTTTCAGCTATNGGCGACTGTGTCGGAGAACAGTAATATGATGTGATTCGTGAA 1759
Oy      572  TYRCYSERHTRGLYASPSERYGLINCYSPPROFROASNLEUNHISLYSGLINASGLY 591
Db      1760  ACGTGCTCGAGAAATTTAAGCCAGCTGTGCCCTTATATATCTTAAATGATGATTTCA 1819
Oy      592  CYSASNGLINASNGLYARGCYSTYRASNGLYGLYCYSLYSTHARGSPASNGLINCYS 611
Db      1820  TGTGATGTGTTCAGGAAATTTGCTTTGGAGAGATGCAAAACAGATAGACAAATGC 1879
Oy      612  GLINTYRILETRPRGLYTHIRLYSALALAGLYSERASPIYSPHECYTYRGLULYSLE 631
Db      1880  AAATACATTTGGGGGCAAAAGGTGACAGCATCAGACAAATATGCTATGAGAACTGAT 1939
Oy      632  THRGLINCILYTHRGLUYSLYASNGLYLYSASPGLYASPARATGTPILLEGINCYSER 651
Db      1940  ATTGAAGGAGCGGAGAGAGGTAACTGTTGGGAAAGCAAGACACATGATACAGTGCAC 1999
Oy      652  LYSNISAPRYALPHECYSGLYPHELEUCYSTHIRASNLEUTHIRARGALAPROARGILE 671
Db      2000  AAACGGGATGCTGTTGTGTTGCTTACCTTTGTGTCACAAATATGGCAATATCCCAAG 2059
Oy      672  GLYGLINLEUGLINCILYGLILETRPHRTHSERPHEHYRTHISGLINLYARGVALILE 691
Db      2060  GGAACACTCGATGTGAAATCACATCTTACTTGTGCGACGAAGGAAGCAATTAAAC 2119
Oy      692  CYSSERGLYALAHISVALLEUVALASPARSPHTRSPVALIGLYTYRVALGLIASPG 711
Db      2120  TGCAGTGTGGGATGTTAAGCTTGAAGAAATGATTAATCTGCTATGTGGAAGATGCG 2179
Oy      712  THRPROCYSGLYPROSERMETCYSLIENUSPARGLYSCYSLAUGLILEGALALEU 731
Db      2180  ACACCTTGCTGTGCTCCCAATGATGTGCTTAGAACACAGGTGTCTTCGCTGCTTCTTC 2239
Oy      732  ASNMETSERCYSPROLEUASPSERYGLYVALCYSSERYGLYNHISGLYVALCY 751
Db      2240  AACTTTAGTCTGCTGACACAGTAAGAACAGCACTATTGCTCAGGAATGGAGTTGC 2299
Oy      752  SERASNGLUALATHRCYSLIECYASPSERHTRPRALAGLYTHRSPCYSSERILEARG 771
Db      2300  AGTATATAGTGAAGTGTGTGTGAACAGACACCTGATGATGCTGATGCTGATGCTG 2350
Oy      772  ASPPROVALARGASNLEUNHISPROPROLYSAPGLULYSPROLYS----- 786
Db      2351  -----AACACTTACTTCCCTACATATGATGCAAAAGACTGATATCACTGTG 2398
Oy      787  -----GLYPROSERALATHRASNLEUILEILEGYSERILEALGLYALALEU 803
Db      2399  TCTGGCAATGCTGTGCTGCGACCAATATCATATATAGCATAAATGCTGCGCACCAT 2458
Oy      804  VALALALALEUVALLEUGLILYTHRGILYRPRGLYRPHLYSASNVALYS 820
Db      2459  GTGCTGCGCTCATATTAAGATAGCTGCGGCTTATTAAGTAAAGTGA 2509

RESULT 10
US-10-170-235-7479
: Sequence 7479, Application US/10170235
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig
: TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
: TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
: FILE REFERENCE: CLO01380
: CURRENT APPLICATION NUMBER: US/10/170, 235
: CURRENT FILING DATE: 2003-03-17
: NUMBER OF SEQ ID NOS: 42514
: SEQ ID NO 7479
: LENGTH: 6753
: TYPE: DNA
: ORGANISM: HUMAN
: US-10-170-235-7479

Alignment Scores:      8.94e-140      Length:      6753
Pred. No.:

```


Db	1940	ATTGAAGGAGCGAGAAAGCGTAACGTGTGGAAAGCAAGACACATGGATACATGCGAAC	1999
Oy	652	LysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIle	671
Db	2000	AAAGGGGATGTGCTTTGTGTACCTTTTGTGTACCAATTAATGGCAATATGCCAACGCTT	2058
Oy	672	GlyGlnLeuGlnGlyGlnIleLeuProHisSerPheGlyThrHisGlnGlyArgValIleAsp	691
Db	2060	GGAGAACTCGATGGCGAATACATCATCTTAAGTTAGTGTGCAGCAAGGAAGAAATTAAC	2119
Oy	692	CysSerGlyAlaHisValLeuAspAspAspThrAspValGlyTyrValGlnAspGly	711
Db	2120	TGCAGTGTGGGCGATGTTAACTGTGAAGAATGTAGACTCTTGGCTATGTGTAAAGATGGG	2179
Oy	712	ThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeu	731
Db	2180	ACACCTTGTTGGTCCCAATATGATGTCTTAGAACACAGGTGTCTTCCGTGGCTCTTTC	2239
Oy	732	AsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCys	751
Db	2240	AACTTACTACTCTGCTTGACGACAGTAAGAAGAACGACATATTGTCTCAGCAAAATGGAGTTGC	2289
Oy	752	SerAsnGlyAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArg	771
Db	2300	AGTATAGAGCTGAAGTGTGTGTGAACAGACACTGGATAGTGTCTGATTTGC-----	2350
Oy	772	AspProValArgAsnLeuHisProProLysAspGlnGlyProLys-----	786
Db	2351	-----AACACTTACTTCCCTCACATATGATATGCAAAGACCTGTGTACTCTGTG	2398
Oy	787	-----GlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGlyValaIleLeu	803
Db	2399	TCTGGCAATGGTGTGCTGCGACCAATATCATTAATAGCATTAATGCTGCGACCATTTTA	2458
Oy	804	ValAlaAlaIleValLeuGlyGlyThrGlyTrpGlyPheLysAsnValLys	820
Db	2459	GTCGTGGCCTCATATTAGGAATTAACGTGCGGTATTAAGTAAGTAAAT	2509
RESULT 11			
US-09-724-676-32237			
Sequence 32237, Application US/09724676			
GENERAL INFORMATION:			
APPLICANT: Comugen LMD			
TITLE OF INVENTION: Variants of alternative splicing			
FILE REFERENCE: 129181.4 Comugen			
CURRENT APPLICATION NUMBER: US/09-724,676			
CURRENT FILING DATE: 2000-11-28			
NUMBER OF SEQ ID NOS: 97222			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 32237			
LENGTH: 2678			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-724-676-32237			

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Alignment Scores:
Pred. No.:      2.74e-140
Score:          1993.50
Percent Similarity: 60.57%
Best Local Similarity: 46.52%
Query Match:    43.78%
DB:
Gaps:          16

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Oy	15	GLYSSSTLEIENALAGLYALASerCysGLYPProGlnArgGLYProAlaGLYSerValPro	34
			:::
Db	15	GGCCCCCGGTGACCCACAGCTGTGTGGCGGACGAGCAAGAGATCCGCGCGCGG	74
Oy	35	AlaSerAlaProAlaArg-----ThrProProCysArgLeuLeu	47
Db	75	GCATGAGAGAGCTGAGCGTCTCGCGGACGAGCGCGCTGACAGCGAGCACTTTCAGG-----	128

QY	48	LeuValIleuLeuLeuLeuProProIleuAlaIleSerSerArgProArgAlaTrpGlyAla	67
Db	129	-----	-CGCGTGGCGTCTG 143
QY	68	AlaAlaIleProSer-----AlaProHisTrpAsnGluThrAlaGluLysAsnLeuGlyVal	85
Db	144	CCGTCGCCCTTCTTTCGCTCTCTGTCTGTCTGGGACCTGCCCTCCGGCGCGC-TGCCGCGCAG	202
QY	86	LeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsnIleSerTySerAsn	105
Db	203	GCAGAGAGCGCTCATTTGATGGAGCTAGAGAAAGAGAGAAAGAAC-----CGC	250
QY	106	AlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyTrpIleAsnGlnAspSer	125
Db	251	TTTCGTGGACCGCCAGAGCATCTCGTACCTGCTTCATTCACCGTCGCGGCGCGAGAAC	310
QY	126	GluSerProTyHisValLeuAspThrLysAlaArgHisGlnGlnLysHisAsnLysAla	145
Db	311	GAAAGTCGGACAGACGCGCTCGACACGCGGCTGGGGGCGACCTCGTGGCGCGCACTTG	370
QY	146	ValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySerLysPheIleLeuAsp	165
Db	371	ACTCATGTGTGACCAAGCAAGCTTCCAGCTTGATGCTTTGGAAAGCATTCATTCGCAT	430
QY	166	LeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyValGluIleHisTyArgLysAsn	184
Db	431	GTCGTGCTAAATCATGATTTGCTGCTCTGATATCATATGACGAGACATTTGAATCGAGA	490
QY	185	GlyLysProGlnTySerLysGlyGluHisCysTyTrpHisGlySerIleArgGly	204
Db	491	GCGAAGACTGTGAAAGTTAAAGAGAGAGACATGTTACTACGAGGCGCATTCGCAAGGA	550
QY	205	ValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGluAsp	224
Db	551	AACCTGACATCTTTGTTGTCATTTGTCATATGCACATGCGACAGCATTCATGAGATGTTCTATGAC	610
QY	225	AspThrPheValIleTyMetIleGluProLeuGluLeuValHisAspGluLysSerThrGly	244
Db	611	GGAAGACACACATCATCTCATTTGAGCCA-----GAAAGAAATGACACTACT	655
QY	245	ArgPro-----HisIleIleGlnLysThrLeuAlaGluIleProLys	259
Db	656	CAAAGAGATTTTCCATTTTTCATTTTCAGTTTACAAATCCAGACTGTTTAAATTTTCCTTGGAT	715
QY	260	-----GlnMetLysAsnLeuThrMetGluLysArgLysAspGlnTrpPro	273
Db	716	GATCTTCCATCTGCATTTTTCAGCAAGATTAACCATTTACTCCATCAAA-----	760
QY	274	PheLeuSerGluLeuGlnIleTrpLeuLysArgArgLysArgAlaValAsnProSerArgGly	293
Db	761	TTTATTTTGAACCAACCAAGCAAAAGGAGACTTAAAGCGACGTTGTCGATATCCTCGTAAT	820
QY	294	IlePheGluGlnMetLysTyLeuGlnLeuMetIleValAsnAspHisLysThrTyLys	313
Db	821	GTAGAGAGAAAGAAACCAAAATACATTGTAACATGATGTGAATCATCACCTTATGTTTAA	880
QY	314	LysHisAspSerSerHisAlaHisThrAspAsnPheAlaLysSerArgValAsnLeuVal	333
Db	881	AAACATCGCGCTTTCCGTTGTACATCCAAATACCTATGCAAAATCTGTGGCAACATGGCA	940
QY	334	AspSerIleTyLysGlnGlnLeuAsnThrArgValValLeuValAlaValGluThrTrp	353
Db	941	GATTTAATATATTAAGAAGACCACTTAAGACAGATATGATTTGGTTCTTATGAAACCTGG	1000
QY	354	ThrGluLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGluPheSer	373
Db	1001	GCGACTGCACACACAGCTTTCCTCATCTGAAATATCCATGTATGACACCTTACGTGAGTTTATG	1060
QY	374	LysTyArgArgGlnArg---IleLysGlnHisAlaAspAlaValHisLeuIleSerArgVal	392
Db	1061	AAATATAGAGAGGAGATTTTATCAAGAGAAAGATGACAGTTCACCTTTTTCGGAACT	1120
QY	393	ThrPheHisTyLysArgSerSerLeuSerTyPheGlnGlyValLysSerArgThrArg	412

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Db 1121 CAATTGAGAGTAGCGGACGGGCGAGCTTATATTGTCGGATTCCTGCTGTAAGA 1180
      ||| ||||| ..... ||||| ||||| |||||
Qy 413 GLYVALGLYALANGLUTRYGLYLEUPROMETALVALAIAAGLVALLEUSERGLINER 432
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1181 GGAGGAGCGCGTGAATGAAATTTGGAAAAGTGAATTTATGGCTTTACCTGCGCCAGTCA 1240
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 433 LEUALAGLANSLEUGLILEGINTRPGLUPROSERARGLYSPROLYS----- 449
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1241 TTACCCATATATTTGGTATT-----ATCCAGACAAGAAAGAAAGTTAGCAAGT 1288
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 450 -----CysaspCysThrGluSerTPRGLYGLYCYSILEMETGLULTRHLYVALSER 467
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1289 GGTGAATGTAATGCGAGACACGTGCTCGCGTCAATATGGAGACACTGCTATTAT 1348
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 468 HISERARGLYSPHERSERLYSCYSERILELEUGLUTRYRARGASPPHELEUGLINARGLY 487
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1349 CTTCCTAAAGAGTTCCACCGAGTAAATTTGAAAGAGTATCATGACTTCCTGGAATAGTGA 1408
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 488 GLYGLYALACYLEUPHEASNARGPROTHRLYLEUPHEGLUPROTHRGLUCYSGLYASN 507
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1409 GGTGGTGGCTGCTTTTCAACAAACCTTTAGCTCTGTGATCCTCGTAGTGGCAAT 1468
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 508 GLYTRYVALGLUALAGLYGLUCYSPCYSGLYPHEHISVALGLUCYSTYR----- 525
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1469 GGCCTTCATTGAACGTGAGAGAGTGTGATTGTGAACCCCGCGCAATGTGCTTGAA 1528
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 526 ---GLYLEUCYSGLYSLYSCYSERILEUSERANGLIANSISYSSERASPGLYPRO 544
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1529 GGAGCAGAGTGTGTGAAGAAATGCACTTGACTCAAGACTCATGACGAGAGAGGTGTT 1588
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 545 CYSYSAASNAANTHRSERCYSLLEUPHEGLINPROARGLYTRYGLUCYSARGASPALAVAL 564
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1589 TGCTGTAA-----AAGTGCAGATTTCACCTTAAGCCACCTGCTGTCGGAAGACAGTA 1642
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 565 ASNGLCYSASPILETHRGLUTRYCYSTRHGLYASPSERGLYGLNLYSPROKASNU 584
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1643 AATGATTTGATATTCGTAACGCTGCTGAGAAATTTAAGCCAGTGTGCCCTAATAT 1702
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 585 HISLYSGINASPGLYTRYALACYSANGLINASNGLYARGCYSTRASNGLYLUCYS 604
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1703 CATTAATAGATGATATTCATGATGATGCTGTCAGGGAATTTGCTTGAGAGAGATGC 1762
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 605 LYSTHRARGASPSANGLINCYSGLINTRYLLETTRPGLYTHLYSALALAGLYSERSPLYS 624
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1763 AAAACGAGATGAGCAATGCAATGCAATTTGGGGCAAAAGTGACACACATCAACAA 1822
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 625 PHECYSTRGLYLSLEUSANTHRGLUGLYTHRGLYLSGLYASNCYSGLYLYSASPGLY 644
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1823 TATTCCTATGAGAACTGAAATTTGAAGGAGCGAGAAAGGTRACGTGTGGAAAGCAAA 1882
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 645 ASPARGTRPILEGINCYSERLYSHISASVALPHECYSGLYPHELEULEUCYSTHRASN 664
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1883 GACACATGATACAGTGCACAAACGAGATGCTGTGGTACTTTGCTTACCAAT 1942
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 665 LEUTHRARGALPROARGILEGLYGLNLEUGLNGLYLLELLEPROTHRSETRHETRYR 684
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1943 ATTCGCAATATCCCAAGCTTGGAGACCTGAGATGCGAATACATCTCTTATGTTGG 2002
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 685 HISGLNGLYARGVALLEASPCYSERGLYALAHISVALLEUSASPSASPTHRASP 704
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2003 CACCAAGGAAGAACATTAACCTCAGTGTGGGACATTTAAGCTTGACAGAAAGTGAAGT 2062
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 705 VALGLYTRYVALGLULASPGLYTHRPROCYSGLYPROSERMETCYSLLEUSASPTARGLYS 724
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2063 CTTCGGCATATGGAAGATGGACACCTGTGGTCCCAATGATGTGCTTAGAAGAACAGG 2122
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 725 CYSLEUGLINTLEGLNALSANSETSERCYSPROLEUSPSERLYSGLYLYSVAL 744
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2123 TGCTTCCTGCTGCTTCTTCACTTACCTTACCTGCTGAGCACTAAAGAGGACTATT 2182
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 745 CYSSECTLYHISGLYVALCYSSERASNGLYALATHRCYSILECYASPSPTHEITRPA 764
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 2183 TGCTCAGGAATGAGATTTCAGTAATGAGTGAAGTGTGCTTAACAGACACTGATA 2242
Qy 765 GLYTHRASPSCYSSERILEARGASPROVALARGASNULEHISPROLYSASPGLY 784
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2243 GGTTCGATTTG-----AACACTTACTTCCCTCACAATATGAT 2281
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 785 PROLYS-----GLYPROSERALATHRASNULEILEILEG 796
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2282 GCAAGACTGTRATCACTGTCTGTGCAATGGTGTGTCGCGCAATATCATTAATAGGC 2341
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 797 SERILEAGLYALALEULEUVALALALALEUVALLEUGLYLYTHCITYRTPGLYR 816
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2342 ATATATTGCGGCACCATTTAGTGTGCGCCCATATTAAGATTAATCTGCGGTAT 2401
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 817 LYSASNVALLYLSYRARG 823
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2402 AAAAATATCGAGAACAGAGG 2422
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-724-676A-32237
: Sequence 32237, Application US/09724676A
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676A
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: patentin version 3.2
: SEQ ID NO 32237
: LENGTH: 2678
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-724-676A-32237

Alignment Scores:
Pred. No.: 2,74e-140 Length: 2678
Score: 1993.50 Matches: 394
Percent Similarity: 60.57% Conservative: 119
Best Local Similarity: 46.52% Mismatches: 252
Query Match: 43.78% Indels: 83
DB: 6 Gaps: 16

US-09-634-252A-4 (1-832) x US-09-724-676A-32237 (1-2678)
Qy 15 GLYCYSERLEUALAGLYALASERCYSGLYPROGLNARGLYPROALGLYSERVALPRO 34
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15 GCGCGCCGCTGAGCCACGCTCTGTTGCGGCGAGCGAAGGAAAGGACTCGCGCGCGG 74
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 35 ALASERALAPROALARG-----THRPROCYARGLEULEU 47
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 75 GCATGAGAGCTGCAGCGTCTCGCGGAGCGCGCTGACGCGACACATGACAGC----- 128
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 48 LEUVALLEULEULEUPROPROLEUALALASERARGLPROARGALATRPGLYALA 67
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 -----CGCAGTGGCTGTGT 143
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 68 ALALAPROSER-----ALAPROHSTRPASNGLUTHRALAGLYLUSANLEUGLYAL 85
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 CCGTCCCTCTTCTGCTCTGTGTGCTGTGGGACTCGCCCTCGGCGCGC-TGGCGCCAG 202
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 86 LEUALASPGLYASPSANTHRLEUGLNGLINASNSERSESRASNILLESERTYISERN 105
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 203 GCAGGACGCGCCCATTTGATGAGCTAGAGAGAGAGAAAGAAAC-----CGC 250
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 106 ALAMETGLNLSGLULLETHRLEUPROSERARGLEULEILETRYTRILEANSGLINSPSER 125
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 TTGCTGAGGCGCCGAGCATTCGTCACCTGCTATTCACCGCTCGGCGCGAGAGC 310
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 126 GLUSERPROLYRHSVALLEUSAPTHRILYSALARGHISGLNGLNLYSHISANLYSALA 145
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 GAAAGTGGGACGAGCGCTGACACGCGGGGTGCGGCGGACCTCGGTGCGCGCAGTTG 370
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[illegible]

Db	1409	GGTGGTGGCTGGCTTTTCAACAAACCTTCAAGCTTCTTGATCCCTCGAGTGGCAAT	1466
Qy	508	GLYTRVALGLUALAGLYLGLUCYSASPCCGLYPHENISVALGLUCYSTYR-----	525
Db	1469	GGCTTCATTTGAACACTGAGAGAGAGTGTGATTTGTGGAACCCGGCCGAATGTCTCTTGA	1526
Qy	526	---GLYLEUCYCYSLYSLYSCYSSERLSEUSERNGLYLAHNSCYSSERASPGLYPRO	544
Db	1529	GGAGCAGAGCTGTGTGAATAATGGCAACCTTGAACCTCAAGACTCTCATATGCAGTGCAGCTT	1588
Qy	545	CYSCYASANAANTHSERCYSLAUMHECINPROARGLYTYRGLUCYARASAPLAVAL	564
Db	1589	TGCTGTAAA-----AAGTGCAGTTTACGCTATGGCACTGTGTGCCGAGAACAGTA	1642
Qy	565	ASNGIUCYASPILETHRGLUTYRCYSTTHRCGLYASPERGLINCYSPPROPSANLEU	584
Db	1643	AATGATTTGTGATATTTCGTGAACACGTGTCAGGAATTCAGCCACTGTGCCCTATATT	1700
Qy	585	HISLYSGIINASPGLYTYRALCYSAASNLINANGIPLYARGCYSTYRASNGLYLCYS	604
Db	1703	CATAAAATGAGTGCATTTATTCATGTGATGGTGTTCAGGCAATTTTCCTTTGGAGAGATGC	1762
Qy	605	LYSTRARASAPASGLINCYSGLTCTYRLLERPPGLYRPLYSALALAGLYSERAPLYS	624
Db	1763	AAACACAGATAGACATGCATAATGCATTTGGGGGCAAAAGTGACACACATCACACAA	1822
Qy	625	PHECYSTYRGIULYSLEUASNTHRCGLIYTHRCGLIULYSGLYASNCYSGLYLYSAPGLY	644
Db	1823	TATTGCTATGAGAAACGTATATTGAAGGACGGAAAGGATACGTGGGAACACAAA	1882
Qy	645	ASPARGTRPILEGINCYSSERLYSHISAPVALPHECYSGLYPHLEULEUCYSTRASN	664
Db	1883	GACACATGTGAATACACTGCACAAACAAAGGGATGGCTTGTGTGTACCTTTTGTTGATCAAT	1942
Qy	665	LEUTHRARGALAPROARGILEGLYGLINLEUNGINGLYGUILLEIAPROTHSERPHERY	684
Db	1943	ATTGGCAATATCCCAAGGCTTGGAGAACTCCATGGTGAATACACTACTACTTTAGTTGTG	2002
Qy	685	HISGLINGIATRVALLIENASPCYSSERGLYLAHNSIVALVALLIENASPASAPTHRASP	704
Db	2003	CAGCAGAGAAAGACATTTAACTGCAGTGGGCGATGTTAAGCTTGAAGAAGATGTAGAT	2062
Qy	705	VALGLYTRYVALGLIINASPGLYTHRPROCYSGLYPROSEMETMELCYSEUASPARGLYS	724
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Qy	725	CYSLEUGINILEGINALALEUASNMESESERCYSPROLEUASPERSELYSGIYLSVAL	744
Db	2123	TGTCCTTCTGTGGCTTCTTTCAACTTTTAGTACTTTCCTTGAGCAGTAAGAAGAGCACTATT	2182
Qy	745	CYSSERGLYHISGLYVALCYSEERASNLUALATHRCYSLIECYASAPHERHTRPVAL	764
Db	2183	TGCTCAGAAATGAGATTGTCAGATGAATGAGTGAAGTGTGTGTGAACAGACATGATTA	2242
Qy	765	GLYTHRASPYSERSELLEARGASPROVALARGASNLEUHSIPROPCOLYSAPGLIUGLY	784
Db	2243	GGTTCGTGATTC-----AACACTTCTTCCTCCACAAATCATAT	2281
Qy	785	PROLYS-----GLYPROSERALATHRASNLEUILEGLY	796
Db	2282	GCMAAGACTGATACACTCTGTCTGCGCAATGTGTGCTGGCACCAATATCATTAATAGGC	2342
Qy	797	SERILELAGIYALALEUVALALALALEVALLEUGIYGLYTHRGLYTRPGLYPHE	816
Db	2342	ATAATTCTGCGCACCATTTTAGTGTGCTGCGCTCATATATAGGAATTAAGTGCCTGGGTTAT	2401
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Mon Jun 2 10:41:06 2003

us-09-634-252a-4.p2n.rnpn

Page 18

job time : 1256 secs

GenCore version 5.1.6
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OW protein - nucleic search, using frame_plus.p2n model

Run on: June 1, 2003, 18:33:56 : Search time 99 Seconds
(Without alignments)
2577.324 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3621	79.5	2268	4	US-09-351-414-1
2	3007	66.0	2088	4	US-09-351-414-3
3	1978	43.4	3183	1	US-08-243-542-8
4	1978	43.4	3183	1	US-08-477-407-8
5	1978	43.4	3183	1	US-08-484-355-8
6	1862.5	40.9	2913	1	US-08-243-542-7
7	1862.5	40.9	2913	1	US-08-477-407-7
8	1862.5	40.9	2913	1	US-08-484-355-7
9	1843	40.5	2923	1	US-08-243-542-6
10	1843	40.5	2923	1	US-08-477-407-6
11	1843	40.5	2923	1	US-08-484-355-6
12	1293	28.4	1464	1	US-08-243-542-5

13	1293	28.4	1464	1	US-08-477-407-5	Sequence 5, Appl1
14	1293	28.4	1464	1	US-08-484-355-5	Sequence 5, Appl1
15	910	20.0	9278	1	US-08-243-542-9	Sequence 9, Appl1
16	910	20.0	9278	1	US-08-477-407-9	Sequence 9, Appl1
17	910	20.0	9278	1	US-08-484-355-9	Sequence 9, Appl1
18	897	19.7	3468	4	US-09-632-098-3	Sequence 3, Appl1
19	871	19.1	3431	1	US-09-632-098-1	Sequence 1, Appl1
20	854	18.8	2968	4	US-09-813-819-1	Sequence 1, Appl1
21	854	18.8	2968	4	US-09-920-048-1	Sequence 1, Appl1
22	829	18.2	2648	2	US-08-836-443-1	Sequence 1, Appl1
23	796	17.5	2251	2	US-08-836-443-2	Sequence 2, Appl1
24	784.5	17.2	2050	4	US-09-026-001A-5	Sequence 5, Appl1
25	773.5	17.0	2335	4	US-09-026-001A-9	Sequence 9, Appl1
26	767.5	16.9	2359	4	US-09-026-001A-17	Sequence 17, Appl1
27	750	16.5	2309	4	US-09-026-001A-13	Sequence 13, Appl1
28	748	16.4	2297	2	US-09-026-001A-7	Sequence 7, Appl1
29	740	16.3	2650	2	US-08-765-243-7	Sequence 7, Appl1
30	740	16.3	2650	5	PCT-US95-07295-7	Sequence 7, Appl1
31	737.5	16.2	1851	4	US-09-608-790-2	Sequence 2, Appl1
32	723.5	15.9	2288	4	US-09-026-001A-11	Sequence 11, Appl1
33	711	15.6	2373	1	US-08-264-101-1	Sequence 1, Appl1
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35	711	15.6	2373	5	PCT-US95-07295-1	Sequence 1, Appl1
36	697	15.3	2553	2	US-08-765-243-5	Sequence 5, Appl1
37	697	15.3	2553	5	PCT-US95-07295-5	Sequence 5, Appl1
38	675.5	14.8	2439	4	US-09-632-098-6	Sequence 6, Appl1
39	647	14.2	2406	4	US-09-632-098-5	Sequence 5, Appl1
40	612	13.4	1820	4	US-09-026-001A-15	Sequence 15, Appl1
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42	588	12.9	2056	2	US-08-836-442-1	Sequence 1, Appl1
43	517	11.4	1768	1	US-08-264-101-3	Sequence 3, Appl1
44	517	11.4	1768	2	US-08-765-243-3	Sequence 3, Appl1
45	517	11.4	1768	5	PCT-US95-07295-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-351-414-1
Sequence 1, Application US/09351414
Patent No. 6265199
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baidur, Nand
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/351,414
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc.feature
LOCATION: (1)...(2268)
OTHER INFORMATION: n = A,T,C or G
US-09-351-414-1
Alignment Scores:
Pred. No.: 4.66e-316
Score: 3621.00
Percent Similarity: 99.70%
Best Local Similarity: 99.70%
Query Match: 79.53%
DB: 4
Length: 2268
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Conservative: 0
Mismatch: 2
Indels: 0
Gaps: 0
US-09-634-252A-4 (1-832) x US-09-351-414-1 (1-2268)

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DB	27	CTTGACACAAAGCGACAGACACCGACGAAAAACATAATTAAGCGCTGCATCTGGCCACGGCA	86
QY	152	SerPheGlnIleGluAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAngly	171
DB	87	AGCTTCCAGATTGAAGCCCTTGGCTCCCAATTCTTGGACTCTTACTGACCAATTCGT	146
QY	172	LeuLeuSerSerAspPheValGluIleHisTyrGluAsnGlyLysProGlnTyrSerLys	191
DB	147	TTGTTGTCTCTCGATTATCTGGAGATTCACTAGAAATATGGAAACACAGTACTGTAAG	206
QY	192	GlyGlyGluHisCysTyrTyrHisGlySerIleArgGlyValLysPheLysValAla	211
DB	207	GGTGAGAGACACTGTTACTACCATGGACATCGAGGCGTCAAGACCTCAAGGTGGCT	266
QY	212	LeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAspPheValTyrMetIle	231
DB	267	CTGTCAACCTGGAAATGGACTTCATCGCATGTTTGAAAGATATACCTTCGTGTATGATA	326
QY	232	GluProLeuGluIleuValHisAspGlyLysSerThrGlyArgProHisIleIleGlnLys	251
DB	327	GAGCCACTAGAGCTGGTTCATGATGAGAAAGACAGCTGACACATATATCCAGAAA	386
QY	252	ThrLeuAlaGlyIleTyrSerLysGlnMetLysAsnLeuThrMetGluArgGlyAspGln	271
DB	387	ACCTTGCGAGAGCAGATATCTTAAGCAAAATCAGAAATCTCACTATGAAAGAGGTACCAG	446
QY	272	ThrProPheLeuSerGluLeuGlnIleProLeuLysArgTyrAspAlaValAspProSer	291
DB	447	TGGCCCTTCTCTGTGAATTACAGTGGTGTGAAAGAAAGAAAGAGACGCTGATCATCA	506
QY	292	ArgGlyIlePheGluGluMetLysTyrLeuGluIleuMetIleValAsnAspHisLysThr	311
DB	507	CGTGGTATATTTCAGAAATGAAATATTGGAACTTATGATTGTAATGATCACAAAAG	566
QY	312	TyrLysLysHisArgSerSerHisAlaHisThrAsnAspPheAlaLysSerValLysn	331
DB	567	TATTAAGAAGCATCCCTCTTCTCAATGCACATCCAAACACTTGGCAAAGTCCGTGGTCAAC	626
QY	332	LeuValAspSerIleTyrLysGlnGlnLeuAsnThrArgValIleValLeuValAlaValGlu	351
DB	627	CTTGTGGATTTCTATTACAGAGAGCAGCTCAACACCAGGCTTCTCTGGTGGCTGTAGAG	686
QY	352	ThrTrpThrGluLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGlu	371
DB	687	ACCTGAGACTGGAAGGATCAGATTGACATCACCAACCAACCTGTGAGATGCTCCATGAG	746
QY	372	PheSerLysTyrArgGlnArgIleLysGlnHisAlaAspAlaValHisIleuIleSerArg	391
DB	747	TTTCCAAATATCCCGCAGCGCATTTAAGCAGCATGCGATGCTGTGACCTCATCTCGCGG	806
QY	392	ValThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyValCysSerArgThr	411
DB	807	GTGAAATTTCACTAATAGAGAGACGACTCGAGTTACTTTGAAAGCTGCTGTCTTCGCACA	866
QY	412	ArgGlyValGlyValAsnGluTyrGlyLeuProMetAlaValAlaGlnValLeuSerGln	431
DB	867	AGAGAGATTGCTGTGAATGATGCTCTTCCAAATGCGATGCGACACAAGATATATCCAG	926
QY	432	SerLeuAlaGlnAsnLeuGlyIleGlnTyrProSerSerArgLysProLysCysAsp	451
DB	927	AGCCCTGGCTCAAAACCTTGGAAATCCAAATGGGAACCTTTAGCGAAAGGCCAAATATGTGAC	986
QY	452	CysThrGluSerThrProGlyCysIleMetGluGluThrGlyValSerHisSerArgLys	471
DB	987	TGCACAGAAATCCCGGGGTGGCTGCATCATGAGAGAAACAGGGGTGCCATTTCGAAAA	1046
QY	472	PheSerLysCysSerIleLeuGluTyrArgAspPheLeuGlnArgGlyGlyValLacys	491
DB	1047	TTTTCAAATGCGACATTTTGGAGTATAGAGACTTTTACAGAGAGAGGTGGAGCCCTGC	1106

OY	492	LeupheasnaRgProthrlYsLeuphegiLupProthGluCySglYAsnGlyTYrvaLslu	511
Db	1107	CTTTTCAACAGCCCAACAAAGCTATTGTGAGCCACCGAATGTGGAAATGATACGTGAA	1166
OY	512	AlaGlyLlulGlySaSpCySGlyPhnHisValGluCySTyrGlyLeuCyScySLys	531
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OY	532	CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCyScySAsnAnThrSerCyS	551
Db	1227	TGTTTCCTCTCCAAAGGGGGCTCACTGACGACGGGGCCCTGGCTGTAACTACCTCATGT	1286
OY	552	LeuphegiLProArGlyTYrGlyLyuCySaArgAspAlaValAsnGluCySAspLleThrglu	571
Db	1287	CTTTTTCAGCCACACAGGGGTGAATGCCGGGATGCTGTGAACGAGTGTATTTACTGAA	1346
OY	572	TyrCySThrGlyAspSerGlyGluCySaProProAsnLeuHisLysGlnAspGlyTYraLa	591
Db	1347	TATTGTACTGGAGACTCTGGTCACTGGCCCAAAATCTTATAGCAAGACGGATTTGCA	1406
OY	592	CysAsnGlnAsnGlnGlyArgCySTyrAsnGlyLyuCySLysThrArgAspAsnGlnCyS	611
Db	1407	TGCATTCAAATCAACAGGCCGCTGGTCACAATGGCAGTGCAGAACACAGACAGCTGAT	1466
OY	612	GlnTYrLleTrrpGlyThrLysAlaAlaGlySerAspLysPheCySTyrGluLysLeuAsn	631
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Db	1587	AAMCAGATGTGTCTGCTGATCTTACTCTGTACCAATCTTACTCGAGCTCCACGATTT	1646
OY	672	GlyGlnLeuGlnGlyGluLleLeuProThrSerPheTYrHisGlnGlyArgValLleAsp	691
Db	1647	GGTCACTTCAGGGGTGAGATCATTTCCAACTTCTCTACCATCAAGCCGGGTGATTTGAC	1706
OY	692	CysSerGlyValAlaHisValLeuAspAspThrAspValGlyTYrValGluAspGly	711
Db	1707	TGCAAGTGGTCCCATGTACTTTAGATGATGATACGGAATGTGGCTATGTAGAGATGGA	1766
OY	712	ThrProCySgLyProSerMetMetCysLeuAspArgLysCysLeuGlnLleGlnAlaLeu	731
Db	1767	ACGGCAATGGTCCCGTCTATGATGATGTTTACATCGGAATGCTCAAAATTCACACCTTA	1826
OY	732	AsnMetSerSerCyProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCys	751
Db	1827	AATTTGAGCAGCTGTCCACTCGATTCGAAGGTAAGTCTTTCCGGGCATCGGGTGTGT	1886
OY	752	SerAsnGluAlaThrCysLleCysAspPheThrTrrpAlaGlyThrAspCysSerLleArg	771
Db	1887	AGTAAATAGCCACTTCATTTTGATATTCACCTGGGACGGACAGATATGCGATTCGGG	1946
OY	772	AspProValArgAsnLeuHisProProLysAspGluGlyProLysGly	787
Db	1947	GATCCAGTAGGAACCTTCACCCCCCAAGAGTAAGAGACCCCAAGGCT	1994
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US-09-351-414-3			
Sequence 3, Application US/09351414			
Patent No. 6265199			
GENERAL INFORMATION:			
APPLICANT: Sheppard, Paul O.			
APPLICANT: Baindur, Nand			
APPLICANT: Delisher, Theresa A.			
APPLICANT: Bishop, Paul D.			
TITLE OF INVENTION: DISINTEGRIN HOMOLOG			
FILE REFERENCE: 98-29			
CURRENT APPLICATION NUMBER: US/09/351,414			
CURRENT FILING DATE: 1999-07-09			

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	LENGTH: 2088	
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	ORGANISM: Artificial Sequence	
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	OTHER INFORMATION: zdin1 amino acid degenerate sequence	
	FEATURE:	
	NAME/KEY: variation	
	LOCATION: (1)...(2088)	
	OTHER INFORMATION: n is any nucleotide	
	FEATURE:	
	NAME/KEY: misc_feature	
	LOCATION: (1)...(2088)	
	OTHER INFORMATION: n = A,T,C or G	
	US-09-351-414-3	
	Alignment Scores:	
	Pred. No.: 7.34e-261	Length: 2088
	Score: 3007.00	Matches: 528
	Percent Similarity: 80.61%	Conservative: 0
	Best Local Similarity: 80.61%	Mismatches: 127
	Query Match: 66.04%	Indels: 0
	DB: 4	Gaps: 0
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DB	88 TTTCARATGACGCGNTTYGCMNSMARITTYATHTTGATYTTNATHTYTNAAAYAGGNTN	147
QY	173 LeuSerSerAspTyrValGluIleHisTyrGluAsnGlyLysProGlnTyrSerLysGly	1929
DB	148 YTNMSMNSMGATYATGCTNCARATHCATYAVGAAAYGNAARCCNCARTRAYMSNAARGN	207
QY	193 GlyGluHisCysTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAlaLeu	2121
DB	208 GGNAGRCATGTYTAT	267
QY	213 SerThrCysAsnGlyLeuHisGlyMetPheGluAspAspThrPheValTyrMetIleGlu	2322
DB	266 WSNACNTGTAAGCAGTNTKATYAGGNAATGTTTGGARGATGATACNTTGTGNTTYATGATHGAR	3277
QY	233 ProLeuGluLeuValHisAspGluLysSerThrGlyArgProHisIleIleGlnLysThr	2525
DB	328 CCNNTYNGARYYTNGTNCATGAYGARAARWSNACNGMNCNCAYTTHATHCARAARACN	367
QY	253 LeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMetGluArgGlyAspGlnTyr	2727
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QY	273 ProPheLeuSerGluLeuGlnTyrPheLysLysArgGlyArgGlyAlaValAsnProSerArg	2922
DB	448 CCNTTYTNTWSMGARYTNCARTCGTYTNAARMGMGNAARMGNCNGTNAAYCCNWSMNGN	507
QY	293 GlyIlePheGluGluMetLysTyrLeuGluLeuMetIleValAsnAspHisLysThrTyr	3121
DB	508 GGNATHTTYTGARGAATGAAATPAAAYTNGCARYTNATGATGNGNAAYCAYCAARACATYAV	567
QY	313 LysLysHisArgSerSerHisAlaHisThrAsnAspPheAlaLysSerValValAsnLeu	3322
DB	568 AARARARCATMGWSMWSNCAAYCCNCAVACNAATAATTTGCCNARWSNCGTNGTNAAYTN	6277
QY	333 ValAspSerIleTyrLysGluGlnLeuAsnThrArgValValLeuValAlaValGluThr	3522
DB	628 GTNGAYWSMATHTTAARARCARATYTNAAAYACMGNGTGTNTTNGTNGCNGTNGARACN	687
QY	353 TrpThrGluLysAspGlnIleAspIleThrThrAsnProValGlnIleLeuHisGluPhe	3727

Db	688	TGGACGAGAAARCAATCATGTAATACNACAACCCCTGCATCATATGTTCATGAATT	
Oy	373	SerLysPArgGlnArgIleValSgInHisAlaAspAlaValHisLeuIleSerArgVal	
Db	748	WSNAARTATATMGNCARRMGNATHAARCACAVCGCAGTCCCTGCATATYTNATHWSMGNTN	
Oy	393	ThrPheHisTyLysArfSerSerLeuSerTyLrPheGlyValCysSerArgThrArg	
Db	808	ACTTTTCATATVAABRGMSNMNSNYTNMTATATTTGCARGNGNTGYNSMGACIMGN	
Oy	413	GlyValGlyValAsnGluTyGlyLeuPrometAlaValAlaGlyValLeuSerGlnSer	
Db	868	GGGTGGTGCTNAATGAARTAYGAGTYNNCCNATGCCCTGCATCNCARGTNTYTNMSCARMSN	
Oy	433	LeuAlaGlnAsnLeuGlyIleGlnTrpGluProSerSerArgLysProLysCysAspCys	
Db	928	YTNGCCCAAATAATYTNCGMATHCARTGGGACRCCKMSNMNGMAARCMAARTGGAATGY	
Oy	453	ThrGluSerTrpGlyLysCysIleMetGluGlyThrGlyAlaSerHisSerArgLysPhe	
Db	988	ACNGARMSTGGGGNGNGNTGYATHATGARGARACACNGNGTNNSCAYNSMGNAARTTY	
Oy	473	SerLysCysSerIleLeuGlnTyTrArgAspPheLeuGlnArgGlyGlyAlaCysLeu	
Db	1048	WSNAARTGYWSNATHYTNCARTRAYMGNGATYYTTCNARBNGNGNGNGCTGYTN	
Oy	493	PheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsnGlyTrvalGluAla	
Db	1108	TTYAAAMGMCNACNARATNTTYTGARCCNACNARGYGGMAYGGNTYATGTMGAGCN	
Oy	513	GlyGluGlyCysAspCysGlyPheHisValGlyCysTyTrGlyLeuGlyCysGLSLysCys	
Db	1168	GGNGARGATGTGCATYGTGGNTTYCAATGTGARTGTAYTGCGTNTNGTGTGAARAATGT	
Oy	533	SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAnthrSerCysLeu	
Db	1228	WSNYTNMSNAAYGCGNCNCATYTGWSNGAYGCGNCMTGYTGAAYAACMSMTGYTN	
Oy	553	PheGlnProArgGlyTrglCysArgAspAlaValAsnGlyCysApIleThrGluTrc	
Db	1288	TTYCACRCMKMGNGNTAYGARITGMYGNGAAGCGTNAAYGARFGYGAATHAACNGARTAY	
Oy	573	CysThrGlyAspSerGlyIncysPropoanLeuHisGlyGlnAspGlyTrglAlaCys	
Db	1348	TGACGNGGATWMSGNCARFTGYCCNCNAAATYTNCAVAAARCARGATGNTATGCTGY	
Oy	593	AsnGlnAsnGlnGlyArgCysTyTrAsnGlyGlyCysLysThrArgAspAsnGlnCysGln	
Db	1408	AAYCARAAVCARCGNMNGNTGYTAAAYGGNGARTGYAARCMNGMNGAYAVCARFTGYCAR	
Oy	613	TyrIleTrpGlyThrLysAlaAlaGlySerAspLysPheCysTyTrGlyLysAsnThr	
Db	1468	TYATATTTGGGNAACNARCGNCGNCGNMSNGAATAATTTGYGAYGARAAARYNAAACN	
Oy	633	GluGlyThrGluLysGlyAsnCysGlyLysAspGlyAspArgTrpIleGlnCysSerLys	
Db	1528	CARGGACMGARARARGMAATYTGCGNAAARGATGGGATYMGNTGGATHCRFTGWSNAAR	
Oy	653	HisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGly	
Db	1588	CAYGAGVTNTTYTGYGNTTYTNTYNTGYACNAAYTTCNMMNGNCGNCCNMGNATHGN	
Oy	673	GlnLeuGlnGlyGluIleLeuProThrSerPheTyHisGlnGlyArgValIleAspCys	
Db	1648	CARYTNACRGGNGARATTHATCCNACMSNTTYTAAVCARCGNMNGNNGNATHGATGY	
Oy	693	SerGlyAlaHisValValLeuAspAspAspThrAspValGlyTrvalGluAspGlyThr	
Db	1708	WSNGGNCMCATGTNTNTNCAATGATGATACMGATGTNCGNATYGTNGBARGATGGNACH	
Oy	713	ProCysGlyProSerMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsn	

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Db      1768  CCNTGYGCGCCNMSNATGATGTGTGTNGATWGNAPRTGYTTCNARATHCAAGCVTNMAY 1827
Oy      733  MetSerSerCysProLeuAspSerLySgLYLySValCysSerGlyHisGlyValCysSer 752
Db      1828  ATGHSMSNSTGTCCTNTNGATWMAAAGGNARAGTNTGYSWNGCAAGGAGTNGTNGYSN 1887
Oy      753  AsnGluIaThrCysIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArgAsp 772
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Oy      773  ProValArgAsnLeuHisProProLysAspGluGlyProLysGly 787
Db      1948  CCNGTNGMAAYTTCATCCNCCNARAGATYARGGNCNNAARGN 1992

RESULT 3
US-08-243-542-8
Sequence 8, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: : EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOETTEL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 MB storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-844470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrylene F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 2308..3183
FEATURE:

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[illegible]

QY 581 oProAsnleuHisLysGlnAspGlyTyrValaCysAsnGlnAsnGlnGlyA:gcysTyrAs 601
D 1572 GCCTAACCTGCACAAAGCTGACGTTACTACTGACATGACGAGGCGCTGACGG 1631
QY 601 nglyGlcysLysThrArgAspAsnGlnCysGlnTyrIleTrrpGlyThrLysAlaAla 621
D 1632 AGCTGCTGCACAAACCCGGGACCGGACGTGCTTTGGGCGCCATCGCGTGC- 1689
QY 621 ySerAspLysPheCysTyrGlnLysLeuAsnThrGlnGlyThrGlnLysGlnCysG 641
D 1690 ----GATCGGCTTCGCTACGAGAGCTGAATGTGAGGAGGACGACCTGAGCTGG 1745
QY 641 yLysAspGlyAspArgTrrpIleGlnCysSerLysHisAspValPheCysGlyPheLeu 661
D 1746 GCGCAAGGAGTCCCGCTGGGTCCAGTGCAGTAACAGAGACGCTGTGTGCTTCCT 1805
QY 661 uCysThrAsnleuThrArgAlaProArgIleGlnGlnLeuGlnGlyGlnIleleProth 681
D 1806 CTGTGTCACACATCTCTGAGCTGCTGCTGAGGAGGAGGAGGAGGAGACATCAGTGTGT 1865
QY 681 rSerPheThrLysGlnGlnLysArgValIleAspCysSerGlyValHisValLeuAspAs 701
D 1866 CACCTTCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1925
QY 701 pasPThrAspValGlyTyrValGlnAspGlyThrProCysGlyProSerMetMetCysLe 721
D 1926 CGGCTCTGACCTGAGTATGTGAGAGTGCACAGCTCCGCGGCTTACATGTGTGCTT 1985
QY 721 uAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysThrLeuAspSerLy 741
D 1986 GGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2045
QY 741 sGlyValaLysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 761
D 2046 GCGCGGATTTGCTCCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2105
QY 761 ethTrrpAlaGlyThrAspCysSerLysArgAspProValArgAsnleuHisProPro- 780
D 2106 AGACTGACAGGCAAAAGCTGACATTCATTAACCCCTGCCACGCTCCACCCACGAG 2165
QY 781 -LysAspGlnGlyProLysGlyProSerAlaThrAsnleuIleIleIleSerIleAlaG 800
D 2166 GGAACGAGAGATATTAAGGTCCAGCGGACGACCAACATCTCATTTGCTCATCGCTGG 2225
QY 800 yAlaIleLeuValAlaAlaIleValLeuGlnGlyThrGlyTrrpGlyPheLysAsnVally 820
D 2226 GGCTGCTCCTGGTTCAGCATCTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2285
QY 820 sLysArgArg 823
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RESULT 5
US-08-484-355-8
Sequence 8, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0

SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 2308..3183
NAME/KEY: CDS
LOCATION: 1..2307
US-08-484-355-8
Alignment Scores:
Pred. No.: 5,78e-168 Length: 3183
Score: 1978.00 Matches: 401
Percent Similarity: 61.69% Conservative: 95
Best Local Similarity: 49.88% Mismatches: 233
Query Match: 43.44% Indels: 76
DB: 1 Gaps: 17
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QY 65 ---TrrpGlyAla-----AlaIleProSerAlaProHisTrrpAsnGlnThrAla 79
D 94 CGATCGGGGGCTTACCCACGCTGGAGGAGCCGACGAGCCCT----- 135
QY 80 GluLysAsnleuGlyValleuAlaAspLysAsnThrLeuGlnGlnAsnSerSer 99
D 135 ----- 135
QY 100 AsnIleSerTyrSerAsnAlaMetGlnLysGlnIleThrLeuProSerArgLeuIleTyr 119
D 136 -----GAGTCACGGAACCAAGCCGCTGCTGTAGG 165
QY 120 TyrIleAsnGlnAspSerGlnSerProTrrpHisValleuAspThrLysAlaArgHisGln 139
D 166 GAG---AGCTCCGGGAGGAGGTCCGAAAGCAGCAGTGCACACAAAGGTCGCCACAGAG 222

OY 140 GlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGly 159
DB 223 CCACAGAGGGGGCCCGCTGCTCATCTGGCCAGAGTGATGTCATCCAGCCCTTAAC 282
OY 160 SerLysPheIleLeuAspLeuIleLeuAsnGlyLeuLeuSerSerAspArgValGlu 179
DB 283 TCMAACTTCACCCCTGGACCTGAGCTGAACCAACCACTCTCTCTCCATACATCTGGAG 342
OY 180 IleHisTyr-----GluAsnGlyLysProGlnTyrSerLysGly---GlyGluHisCysTyr 197
DB 343 GCCCACTTCAGCCGGGAGGGAGCAACCAACGACACACCGGGGCTGGAGACCACTGCTAC 402
OY 198 TyrHisGlySerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGly 217
DB 403 TACAGAGGGGAACCTCCGGGGGAACCCGACCTCTCCGCGCCCTCCACCTCCAGAGGG 462
OY 218 LeuHisGlyMetPheGluAspAspThrPheValTyrMetIleGluProLeuGluVal 237
DB 463 CTGCATGGGGCTCTCTGATGGAACTTGACTTACATGATGAGGCCCAAGAGGTGCT 522
OY 238 -----HisAspGluLysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGly 255
DB 523 GGAACCTTGGGGAGCCCTCAGAGACCCCTCCCACTCATTTACCGGAGCCCTCTCT 581
OY 256 GlnTyrSerLysGlnMetLysAsnLeuThrMetGluArgGlyAspGlnTyrPro-PheLe 275
DB 582 CCCAGATCCCTCGGATG-----CAGGAAACCGAGCTCTGTTGCT 623
OY 275 uSerGluLeuGlnTyrLeuLys-----ArgArgLysArgAlaValAs 289
DB 624 TGTGCTGCCCATCGCTCTCCAAACCGCGGAGCTGAGAAAGGAAGGAGGTCCG 683
OY 289 nProSerArgGly-----IlePheGluGluMetLysTyrLeuGluLeuMetIleVal 306
DB 684 C-----CGGGGCAACCTCAGTACGACGACGAAACCAAGTATGATGATTTGGAT 737
OY 306 LAsnAspHisLysThrTyrLysHisArgSerSerHisAlaHisThrAsnAspHeal 326
DB 738 CAACGACACACAGCTGTTCAGCAGCAGATGCGAGCTCGGTGCTCAACCACTTTC 797
OY 326 LysSerValValAsnLeuValAspSerIleTyrLysGluGlnLeuAsnThrArgVal 346
DB 798 CAAGTCCGTGGTGAACCTGGCCGATGATACAGAGAGAGCTCAACACTCCATCGT 857
OY 346 IleValAlaValAlaGluThrTyrThrGluLysAspGlnIleAspIleThrTrpAsnProVal 366
DB 858 CTGTGTTGCCATGGAAACATGGGACATGGGACAAATCCAGTGCAGATGACTCT 917
OY 366 LglMetLeuHisGluPheSerLysTyrArgGlnArg---IleLysGlnHisAlaAspAl 385
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OY 385 aValHisLeuLeuSerArgValAlaThrPheHisTyrLysArgSerSerLeuSerTyrPheG 405
DB 978 CACCACTCTCTTCGCGGAGAGACCTTCAGAGCAGAGAGCGGGGAGAGCTACGTGGG 1037
OY 405 yGlyValCysSerArgThrArgGlyValAlaGlyValAsnGluTyrGlyLeuProMetAlaVal 425
DB 1038 GGGCATATGCTCCCTGCTCCAGGCGGGGCTGTGAACAGTAACGCAACATGGGGGCAAT 1097
OY 425 lAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTyrP---GluProSe 444
DB 1098 GGCCCTGACCTTGGCCAGAGCCCTGAGACAGAACCTGGGATGATGTGAAACAAACCCG 1157
OY 444 rSerArgLysProLysCysAspCysThrGluSerThrGlyGlyCysIleMetGluGluThr 464
DB 1138 GAGCTCGGAGGAGGAGTGAAGTGTCCAGACATCTGCTGGGCTGATCATGAGAGACAC 1217
OY 464 rGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyrArgAspPheLe 484
DB 1218 TGGGTTTCTACCTGCCCCGCAAGTCTCTGCTGACAGCATGCAAGATCAACCAAGTTTCT 1277

OY 484 uGlnArgGlyGlyAlaCysLeuPheAsnArgProThrLysLeuPheGlnProThrGln 504
DB 1278 GCAGAGGGGTGTGACACTGCTCTTCACAAACCCCTCAAGGTCTGAGACCCCAAGA 1337
OY 504 uCysGlyAsnGlyTyrValAlaGluAlaGlyGluCysAspCysPheHisValGluCys 524
DB 1338 GTCCGGGAACGGCTCTGGAGGAGGAGGAGATGACACTGCGGCTCGGTCGAGAGATG 1397
OY 524 sTyr-----GlyLeuCysCysLysLysCysSerLeuSerAsnGlnAlaHisCysSe 541
DB 1398 CAGCCCGCAGGTGGCACTGCTGCAGAAATGCACCCCTGACTCAGACGCGCATGTGAG 1457
OY 541 rAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProAlaGlyTyrGluCysArg 561
DB 1458 GCAGGGGCTCTGCTGCGCCG-----TGCAGATACAGAACCAAGGCTGTCTCTGCG 1511
OY 561 gAspAlaValAsnGluCysAspIleThrGlnLysTyrCysThrGlyAspSerGlyGlnCysPr 581
DB 1512 AGAGCGCTGAAACGAGTGCAGATGCGGAGACTGCGAGACTGACCGGGACTCAAGCACTGCC 1571
OY 581 oProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyrAs 601
DB 1572 GCCTAACCTGCACAACTGGAGGTGATGATGATGATGATGATGATGATGATGATGATG 1631
OY 601 nGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleThrPrgLysThrLysAlaAlaG 621
DB 1632 AGCTCGCTCAAAACCCGGAGCGGAGCGGAGCGGAGGTTCTTGGGCGCATGCGGCTCT-- 1689
OY 621 ySerAspLysPheCysTyrGluLysLeuAsnThrGlnGlyThrGluLysGlyAsnGly 641
DB 1690 ---GATCGCTTGTGTACAGAACTGAAATGAGAGGGAGGAGGAGGAGGAGGAGGAGG 1745
OY 641 yLysAspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeuLe 661
DB 1746 GCGCAAGGATCGCGGCTGAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 1805
OY 661 uCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyGluIleLeuProTh 681
DB 1806 CTGTGTCACATCTCTGAGCTCTCGGCTAGGAGGAGCTGCTGGAGACATCACTAGTCT 1865
OY 681 rSerPheThrHisGlnGlnArgValAlaAspCysSerGlyAlaHisValValLeuAspAs 701
DB 1866 CACCTTCTACACACAGGCAAGAGCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1925
OY 701 pAspThrAspValGlyTyrValAlaGluAspGlyThrProCysGlyProSerMetLysLe 721
DB 1926 CGGCTGACCTGAGTATGAGGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 1985
OY 721 uAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSerL 741
DB 1986 GGACCATCGCTGCTGCGAGCTTCTGCTTCACTTCAAGCACTGCCCCGGCACTGGGGA 2045
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DB 2046 GCGCGGATTCCTCCACCAACGAGGCTGCGAGCATGAGCAATGAAGAAAGTCACTGCTCAG 2105
OY 761 eThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro-- 780
DB 2106 AGACTGAGCAGGCAAAAGCTCAGATTCATCAACCCCTGCCACGCTCCCAACCCAGCG 2165
OY 781 -LysAspGluLysProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaG 800
DB 2166 GAGACGAGAGATTAAGGTCCAGCGGAGCAGCAACATCATATGGCTCATGCTGCGGG 2225
OY 800 lAlaIleLeuValAlaAlaIleValAlaGlyGlyGlyThrGlyThrGlyPheLysAsnVal 820
DB 2226 GCGTCTCTGCTGAGCCATGCTCTGCGGCGGAGCGGCTGGGATTAATAAATTCG 2285
OY 820 sLysArgArg 823
DB 2286 CCGAGAGAG 2295
RESULT 6

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US-08-243-542-7
: Sequence 7, Application US/08243542
: Patent No. 5552526
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: APPLICANT: : EMI, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAS
: TITLE OF INVENTION: ENCODING THE SAME
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLYNN, THEL, BOUTELL & TANIS P.C.
: STREET: 2026 Rambling Road
: City: Kalamazoo
: STATE: Michigan
: COUNTRY: USA
: ZIP: 49008-1699
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
: COMPUTER: IBM PC/XT/AT Compatible
: OPERATING SYSTEM: MS-DOS 5.0
: SOFTWARE: WordPerfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/243,542
: FILING DATE:
: CLASSIFICATION: 530
: PRIORITY INFORMATION:
: APPLICATION NUMBER: JP 5-136602
: FILING DATE: 14 MAY 1993
: APPLICATION NUMBER: JP 5-257455
: FILING DATE: 22 SEPTEMBER 1993
: APPLICATION NUMBER: JP 6-49904
: FILING DATE: 23 FEBRUARY 1994
: APPLICATION NUMBER: JP 6-73328
: FILING DATE: 12 APRIL 1994
: APPLICATION NUMBER: JP 6-84470
: FILING DATE: 22 APRIL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Teriyence F. Chapman
: REGISTRATION NUMBER: 32 549
: REFERENCE/DOCKET NUMBER: Furuya Case 1313
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (616) 381-1156
: TELEFAX: (616) 381-5465
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2913 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: LIBRARY: human fetal brain cDNA library
: FEATURE:
: NAME/KEY: 5' UTR
: LOCATION: 1..27
: FEATURE:
: NAME/KEY: 3' UTR
: LOCATION: 2038..2913
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 28..2037
: US-08-243-542-7

Alignment Scores:
Pred. No.: 1,24e-157 Length: 2913
Score: 1862.50 Matches: 360
Percent Similarity: 66.72% Conservative: 91
Best Local Similarity: 55.22% Mismatches: 193
Query Match: 40.91% Indels: 33
GB: 1 Gaps: 13

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QY 187 ProGlnTyrSerLysGly---GlyGlnHisCysTyrTyrHisGlySerLeuArgGlyVal 205	187 ProGlnTyrSerLysGly---GlyGlnHisCysTyrTyrHisGlySerLeuArgGlyVal 205
Db 97 ACCAGCACACACCGGGGGCTGGAAACACACTCTACTACACAGGGGAAGCTCCGGGGAGAAC 156	97 ACCAGCACACACCGGGGGCTGGAAACACACTCTACTACACAGGGGAAGCTCCGGGGAGAAC 156
QY 206 LysAspSerLysValAlaLeuSerThrcCysAsnGlyLeuHisGlyMetPheGluAspAsp 225	206 LysAspSerLysValAlaLeuSerThrcCysAsnGlyLeuHisGlyMetPheGluAspAsp 225
Db 157 CCGACACTCTTGGCGCCCTCTCCACACCTGCCAGGGGCTGCATGGGGTCTTCTCTATGG 216	157 CCGACACTCTTGGCGCCCTCTCCACACCTGCCAGGGGCTGCATGGGGTCTTCTCTATGG 216
QY 226 ThrPheValTyrMetIleGluProLeuGluLeuVal-----HisAspGluLysSerThr 243	226 ThrPheValTyrMetIleGluProLeuGluLeuVal-----HisAspGluLysSerThr 243
Db 217 AACTTGATGATCATCATCTGGAGCCCCCAAGAGGGCTGGACCTTGGAGGCCCTCAGGA 276	217 AACTTGATGATCATCATCTGGAGCCCCCAAGAGGGCTGGACCTTGGAGGCCCTCAGGA 276
QY 244 GlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsn 263	244 GlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsn 263
Db 277 CCCCCTCCCACTCATTTACCCGAGCCCC-TCCTCTCCAGATCCCTCCGCGATG----- 329	277 CCCCCTCCCACTCATTTACCCGAGCCCC-TCCTCTCCAGATCCCTCCGCGATG----- 329
QY 264 LeuThrMetGluArgGlyAspGlnTyrPro-PheLeuSerGluLeuGlnTyrLeuLys-- 282	264 LeuThrMetGluArgGlyAspGlnTyrPro-PheLeuSerGluLeuGlnTyrLeuLys-- 282
Db 330 -----CAAGAACACAGGCTGCTGTTTCTCTGCTGCTGCCCACTGCGCTCTCC 377	330 -----CAAGAACACAGGCTGCTGTTTCTCTGCTGCTGCCCACTGCGCTCTCC 377
QY 283 -----ArgArgLysArgAlaValAsnProSerArgGly-----I 294	283 -----ArgArgLysArgAlaValAsnProSerArgGly-----I 294
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QY 294 ePheGlnGluMetLysTyrLeuGlnLeuMetIleValAsnAspHisLysTyrThrTyrLys 314	294 ePheGlnGluMetLysTyrLeuGlnLeuMetIleValAsnAspHisLysTyrThrTyrLys 314
Db 432 GCACAGTAAACCAAGTGTGTGGACCTAAATTGTGTATCAACGCCACCAACAGCTGTTCAGACA 491	432 GCACAGTAAACCAAGTGTGTGGACCTAAATTGTGTATCAACGCCACCAACAGCTGTTCAGACA 491
QY 314 sHisArgSerSerHisAlaHisIleThrAspAsnPheAlaLysSerValValAsnLeuValAs 334	314 sHisArgSerSerHisAlaHisIleThrAspAsnPheAlaLysSerValValAsnLeuValAs 334
Db 492 GATCGACAGACGTGCGGTGCTCTACACAGCAACTTTCACAAAGTCGTTGGTGAACCTGGCCGA 551	492 GATCGACAGACGTGCGGTGCTCTACACAGCAACTTTCACAAAGTCGTTGGTGAACCTGGCCGA 551
QY 334 pSerIleTyrLysGlnLeuAsnThrArgValValLeuValAlaValGluThrTyrPth 354	334 pSerIleTyrLysGlnLeuAsnThrArgValValLeuValAlaValGluThrTyrPth 354
Db 552 TGTGATATACAAAGGAGCGACTCAACACTCGCATGCTCTGGTTCCTCATGAAACATGGGC 611	552 TGTGATATACAAAGGAGCGACTCAACACTCGCATGCTCTGGTTCCTCATGAAACATGGGC 611
QY 354 rGluLysAspGlnIleAspIleThrThrAsnProValGluMetLeuHisGluPheSerLys 374	354 rGluLysAspGlnIleAspIleThrThrAsnProValGluMetLeuHisGluPheSerLys 374
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Db 672 CTACCGAGGGAGGAGGCTGCTGAGCCAGCAATTCACCCCACTCTTCTGGGGCAGAGC 731	672 CTACCGAGGGAGGAGGCTGCTGAGCCAGCAATTCACCCCACTCTTCTGGGGCAGAGC 731
QY 393 rPheHisTyrLysArgSerSerLeuSerTyrPheGlyValCysSerArgThrArgG1 413	393 rPheHisTyrLysArgSerSerLeuSerTyrPheGlyValCysSerArgThrArgG1 413
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QY 452 sThrGluSerTyrPheGlyCysIleMetGlnGluThrGlyValSerHisSerArgLysPh 472	452 sThrGluSerTyrPheGlyCysIleMetGlnGluThrGlyValSerHisSerArgLysPh 472
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QY 472 eSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGlyGlyGlyAlaCysLe 492	472 eSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGlyGlyGlyAlaCysLe 492
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QY 492 uPheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrValGluAl 512	492 uPheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrValGluAl 512
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QY 769 fileargaprovealargasnleuhspropro----lysaspgluclyprolysglypr 788
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QY 788 oseralathrasnleuileileglyserllealaglyalaleuavalaleuavalaleuava 808
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Db 1980 CCGTGGCGGACGCGGCTGGGATTTTAAACATTTGCGGAGGAGGAGG 2025

RESULT 7

US-08-477-407-7
; Sequence 7, Application US/08477407
; Patent No. 561351
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YOSUKE
; APPLICANT: EMI, MITSURU
; TITLE OF INVENTION: MDC PROTEINS AND DNAs

TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THELL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrylene F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2913 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: 5' UTR
LOCATION: 1..27
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 2038..2913
FEATURE:
NAME/KEY: CDS
LOCATION: 28..2037
US-08-477-407-7
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Score: 1862.50 Matches: 360
Percent Similarity: 66.72% Conservative: 91
Best Local Similarity: 53.25% Mismatches: 193
Query Match: 40.91% Indels: 33
Gaps: 13
DB: 13
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Db 37 CTGAGCAGCAGCT 96

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Db	97	ACCCAGCAGACACCGGGGCTGGAGACCACTGCTACTACCAAGGGAGACACTCGGGGGAAC	156
OY	206	LysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGlnuAspAsp	225
Db	157	CCGCACTCTCTGGCGCGCCCTCTCCACCGCAGGGGCTGCATGGGGGTCTTCTCATGTGG	216
OY	226	ThrPheValYrMetIleGluProLeuGluLeuVal-----HisAspGluLysSerThr	243
Db	217	AACTTGACTTCATACGTGGAGCCCCAGAGGGTGGCTGGACCTTGGGGAGCCCCTCAGAGA	276
OY	244	GlyArgProHisIleIleGlnThrLeuAlaGlyGlnTrpSerLysGluMetLysAsn	263
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Db	330	-----CAGGGAACAGGCTGCTGTGGTGGCTGGCTGGCAGTCGGGTCCCTCC	377
OY	283	-----ArgArgLysArgAlaValAsnProSerArgLy-----I	294
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OY	314	SHisArgSerSerHisAlaHisThrAsnAsnPheAlaLysSerValValAsnLeuValAs	334
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OY	334	PSerIleTyrLysGluGlnLeuAsnThrArgValValLeuValAlaValGluThrTrpTh	354
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Db	612	AGATGGGGACAAAGTCCAGTCCAGTGCAGAGTACCTCTCTGGAGACCTGGGCCCTCATGTGT	671
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OY	413	yValGluValAsnGlnTyrGlyLeuProMetAlaValAlaGlnValLysSerGlnSerLe	433
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OY	452	SThGluSerTrpGlyLysIleMetGlnGluThrGlyValSerHisSerArgLysPhe	472
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[illegible]

US-08-484-355-7
 : Sequence 7, Application US/08484355
 : Patent No. 5705341
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: MAKAMURA, YUSUKE
 :
 : APPLICANT: EMI, MITSURU
 :
 : TITLE OF INVENTION: MGC PROTEINS AND DNAS
 :
 : TITLE OF INVENTION: ENCODING THE SAME
 :
 : NUMBER OF SEQUENCES: 20
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: FUJIN, THEIL, BOUTELL & TANIS P.C.
 :
 : STREET: 2026 Rambling Road

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 1, 2003, 18:52:31 : Search time 302 Seconds

(without alignments)
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Delop 6.0 , Delext 7.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3621	79.5	2268	10	US-09-809-617-1	Sequence 1, Appli
4	3007	66.0	2088	10	US-09-809-790-3	Sequence 3, Appli

5	3007	66.0	2088	10	US-09-809-617-3	Sequence 3, Appli
6	1680	36.9	1668	10	US-09-792-200B-17	Sequence 17, Appli
7	1029.5	22.6	3512	9	US-10-020-733-9	Sequence 9, Appli
8	1016.5	22.3	6488	9	US-10-161-803-48	Sequence 48, Appli
9	1012.5	22.2	6475	9	US-10-161-803-49	Sequence 49, Appli
10	1007.5	22.1	2757	9	US-10-020-733-3	Sequence 3, Appli
11	1007.5	22.1	2757	9	US-10-125-470-2	Sequence 2, Appli
12	1007.5	22.1	2757	9	US-10-125-452-2	Sequence 2, Appli
13	1007.5	22.1	2757	9	US-09-955-504-2	Sequence 2, Appli
14	1007.5	22.1	2781	9	US-10-020-733-1	Sequence 1, Appli
15	1007.5	22.1	2868	9	US-10-020-733-7	Sequence 7, Appli
16	1007.5	22.1	2892	9	US-10-020-733-5	Sequence 5, Appli
17	982	21.6	1674	10	US-09-792-200B-15	Sequence 15, Appli
18	981	21.5	7920	12	US-10-044-090-781	Sequence 781, App
19	978	21.5	6352	10	US-09-983-531A-3	Sequence 3, Appli
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					US-10-176-492-87	Sequence 87, Appli

ALIGNMENTS

RESULT 1
US-09-824-129-2
Sequence 2, Application US/09824129
Patent No. US20020001840A1
GENERAL INFORMATION:
APPLICANT: Lopez-Otin, Carlos
APPLICANT: Miguell, Santiago Cal
APPLICANT: Freije, Jose Maria Perez
APPLICANT: Garcia, Jose Manuel Lopez
APPLICANT: Bianchi, Albert Bernard
APPLICANT: Trail, Pamela
TITLE OF INVENTION: Methods and Compositions for Modulating
Integrin-mediated Cell-Cell Interactions
FILE REFERENCE: D0015-NP
CURRENT APPLICATION NUMBER: US/09/824,129
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/194,164
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4043
TYPE: DNA
ORGANISM: Homo sapiens
US-09-824-129-2
Alignment Scores: 0
Pred. No.: 0
Length: 4043

Score: 4553.00 Matches: 832
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-634-252a-4 (1-832) x US-09-824-129-2 (1-4043)

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DB 1017 ATGAAGCGCCCGGAGAGCTCGCGGAGCGCCCGGCGGCTGAGCTTCCGGC 1076
QY 21 AlasrCysGlyProGlyArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
DB 1077 GCTTCTCGGGCCCGCCAAAGCGGCGCCCGGCTGGTGCTCGCAGCGCCCGCGCCG 1136
QY 41 ThrProCysArgLeuLeuLeuValLeuLeuLeuProProLeuAlaAlaSerSer 60
DB 1137 AGCGCGCCCTGGCGCTGCTCTCGCTCTCTCGCTCTCGCTCTCGCTCTCGCTCT 1196
QY 61 ArgProAlaGlyAlaTrrGlyAlaAlaAlaProSerAlaProHisTrrAsnGlyThrAlaGlu 80
DB 1197 CGCGCCCGGCTGGGGGCTGCTCGCGCCAGCGCTCCGATTTGGAATGAATGAGAA 1256
QY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100
DB 1257 AAAAATTTGGAGCTCTGGCAGATGAAGCAATACATTGCACAGAAATGACAGCAATA 1316
QY 101 LLeSerTrrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTrrYr 120
DB 1317 ATCAGTTACAGCAATGCAATGCAAGAAAGAAATCCACTGCTTCAAGACTCATATATT 1376
QY 121 LLeAsnGluAspSerLeuSerProTrrHisValLeuAspThrLysAlaArgHisGln 140
DB 1377 ATCAACCAAGACTCGGAAAGCCCTTATCACGTTCTTGACCAAAAGCCAGACAGCA 1436
QY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160
DB 1437 AAACATTAATAGGCTGCTGCATCTGGCCAGCAAGCTTCAGATTGAAAGCTTCGCTCC 1496
QY 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTrrValGluIle 180
DB 1497 AAATTCATCTTACCTCACTACATGAAACAAATGTTGTGTTCTTGATTAATGAGAA 1556
QY 181 HisTrrGluAsnGlyLysProGlnTrrSerLysGlyLysGlnHisCysTrrYrHisGly 200
DB 1557 CACTAGCAAAATGGAGAACACACAGTACTTAAAGGTGAGAGACACTTACTACATGGA 1616
QY 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220
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QY 221 MetPheGluAspAspThrPheValTrrMetIleGluProLeuGluValHisAspGlu 240
DB 1677 ATGTTTAAAGTGTATACCTTCGTGTATATGATAGACCACTAGAGCTGGTTCATGAT 1736
QY 241 LysSerThrGlyArgProHisIleIleGlnTrrThrLeuAlaGlyGlnTrrSerLysGln 260
DB 1737 AAAAGCACAGGTGCACCATATATATCCAGAAACCTTGGCAGGAGCACTATTTCAAGCA 1796
QY 261 MetLysAsnLeuThrMetGluArgGlyLysAspIleTrrProPheLeuSerGluLeuGlnTrr 280
DB 1797 ATGAAGATTCACATATGAGAAAGGTGACCAAGTGGCCCTTCTCTGCAATTCACAG 1856
QY 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlnGluMetLysTrr 300
DB 1857 TTGAAATAAGCAAGAGAGAGTGAATCAGTCACTGATATATTGAAAGAAATGAATAT 1916
QY 301 LeuGluLeuMetIleValAsnAspHisLysTrrYrLysHisArgSerSerHisAla 320
DB 1917 TTGAACTTATGATGTTATATGATCACAAGCGTAAAGAACATCGCTTCTCATGCA 1976
QY 321 HisTrrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTrrYrLysGluGln 340

DB 1977 CATACCAACAACTTGGCAAGTCCGTGTCAACCTTGATTCATTTACAAAGACAG 2036
QY 341 LeuAsnTrrArgValValLeuValAlaValIleThrTrrPrrGluLysAspGlnIleAsp 360
DB 2037 CTCAACACACAGGTTGCTCGTGTGCTGAGAGACTTCGACTGCAAGAGATCAATTCAC 2096
QY 361 ThrTrrAsnProValGlnMetLeuHisGluPheSerLysTrrArgGluArgIleLys 380
DB 2097 ATCAACCAACAACTTGGCAAGTCCGTGTCAACCTTGATTCATTTACAAAGACAG 2156
QY 381 GlnHisAlaAspAlaValHisLeuIleSerArgValIlePheHisTrrLysArgSerSer 400
DB 2157 CAGCATGCTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2216
QY 401 LeuSerTrrPheGlyLysValLysSerArgTrrArgGlyValGlyValAsnGlyTrrGly 420
DB 2217 CTGAGTTACTTGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2276
QY 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440
DB 2277 CTTCCAATGCGAGTGGCACAGTATTTATGCGAGAGCTGGCTCAAAACCTTGGAA 2336
QY 441 TrrGluProSerSerArgLysProLysCysAspCysThrGluSerTrrGlyLysCysIle 460
DB 2337 TGGGAACCTTTCTACGCAAGAAAGCCAAATGTAAGTCAAGAAATTCCTGGGCTG 2396
QY 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGlyTrr 480
DB 2397 ATGAGAGAAACAGGCTGCCATTCCTCAAAATTTTCAAAAGCGAGCATTTTGGAGTAT 2456
QY 481 ArgAspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsnArgProThrLysLeuPhe 500
DB 2457 AGAGACTTTTACAGAGAGAGGAGGAGCTGCTTTTCAACAGGCGCAACAAAGCAT 2516
QY 501 GluProThrGluCysGlyAsnGlyTrrValGluAlaGlyLysLysAspCysGlyPhe 520
DB 2517 GAGCCACGGAATCTGGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2576
QY 521 HisValGluCysTrrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540
DB 2577 CATGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2636
QY 541 SerAspGlyProCysAsnAsnThrSerCysLeuPheGlnProArgGlyTrrGluCys 560
DB 2637 AGCGAGCGGCTGCTGTAAACATCTCATGCTTTTTCAGCCAGGAGGTATGATGTC 2696
QY 561 ArgAspAlaValAsnGluCysAspIleThrGluTrrCysThrGlyAspSerGlyLys 580
DB 2697 CGGATGCTGTGAACGAGTGTGATATTAAGTAATATTGACTGAGACTGTGCTCACTGC 2756
QY 581 ProProAsnLeuHisLysGlnAspGlyTrrAlaCysAsnGlnAsnGlnArgCysTrr 600
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QY 601 AsnGlyGluCysLysTrrArgAspAsnGluCysGlnTrrIleTrrPrrGlyThrValAla 620
DB 2817 AATGGCAGTCAAGACACAGACACAGAGTGTGATGATGATGATGATGATGATGATGAT 2876
QY 621 GlySerAspLysPheCysTrrGluLysLeuAsnThrGluGlyThrGluLysGlyAsnCys 640
DB 2877 GGGTGTGACAACTTCTGTATGAAGAAAGTGAATACAGAAAGCACTGAAAGAAAGCA 2936
QY 641 GlyLysAspGlyAspArgTrrIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660
DB 2937 GGAAGAGATGAGAGCGGCTGATTCAGTCAAGCAACATGATGTGTTCTTGAGATTCCT 2996
QY 661 LeuCysTrrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyLysIleLeuPro 680
DB 2997 CTCTGTACATCTTACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3056
QY 681 ThrSerPheTrrHisGlnGlyArgValIleAspCysSerGlyAlaHisValValLeuAsp 700

Dh 3057 ACTTCCTTACCATCAGAGCCGGGTGATTGACTGCAGTGGTCCCATGTAGTTTACAT 3116
Oy AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720
Dh 3117 GATGATACGGATGTGGCTATGTAGATGAGAACCCATGTGGCCGCTATGATGTGT 3176
Oy LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740
Dh 3177 TTAGATCGGAGAGCTTACAAATTCAGGCCCTAAATATGAGCAGCTGTCCACATTC 3236
Oy LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760
Dh 3237 AAGGGTAAAGTCTGTTCGGGCCATGGGCTGTAGTAATGAACCCATCTGCATTTGTGAT 3296
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Dh 3297 TTCACCTGGGACAGGACAGATTTCAGTATCCGGGATTCAGTTAGGAACCTTCACCC 3356
Oy LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
Dh 3357 AAGCATGAAGAGCACCAGGGTCTTACAGCCCAATCTCATATAGGCTCATCGGTGT 3416
Oy AlaIleLeuValAlaIleValIleValIleValGlyTyrGlyTrrProGlyPheLysAsnValLys 820
Dh 3417 GCCATCCTGGTACACCTATTTGCTTGGGGCAGAGGGGATTTAAATAATGTCAG 3476
Oy LysArgArgPheAspProThrGlnGlnGlyProIle 832
Dh 3477 AAGAGAAGTTCGATCTCTACTCAGCAAGCCCATC 3512

RESULT 2
US-09-809-790-1

Sequence 1, Application US/09809790
Patent No. US20020072102A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Balindur, Nand
APPLICANT: Delisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/809,790
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc_feature
LOCATION: (1)...(2268)
OTHER INFORMATION: n = A,T,C or G
US-09-809-790-1

Alignment Scores:

Pred. No.: 0 Length: 2268
Score: 3621.00 Matches: 654
Percent Similarity: 99.708 Conservative: 0
Best Local Similarity: 99.708 Mismatches: 2
Query Match: 79.538 Indels: 0
DB: 10 Gaps: 0

US-09-634-252a-4 (1-832) x US-09-809-790-1 (1-2268)

Oy 132 LeuAspThrLysAlaArgHisGlnGlnLysHisAsnLysAlaValAlaHisLeuAlaGlnAla 151
Dh 27 CTTGACACAAAGGCAAGACACACCAACAAACATATATAGGCTGTGCCATGGCCAGGCA 86

Oy 152 SerPheGlnIleGlnAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnGly 171
Dh 87 AGCTTCAGATTGAAGCTTCGGCTCCCAATTCATTCTTGACCTCATACATGCAACATGCT 146
Oy 172 LeuLeuSerSerAspTyrValGluIleHisTyrGluAsnGlyLysProGlnTyrSerLys 191
Dh 147 TTCTGTCTCTGATTAATGAGAGATTCACTAGCAAAATGCGAAACACAGTACTTAAG 206
Oy 192 GlyGlyGlnHisCysTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAla 211
Dh 207 GGTGGAGAGCAGCTGTACTACCATGAGAGCATCAGAGGCTCAAGACTCCAAAGGTGGCT 266
Oy 212 LeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAspThrPheValTyrMetIle 231
Dh 267 CTGTCAACCTGCATGAGCATCTTCATGGCATGTTTGAAGATGATACCTTCGTTATGATA 326
Oy 232 GluProLeuGlnLeuValHisAspGlyLysSerThrGlyArgProHisIleIleGlnLys 251
Dh 327 GAGCCACTAGAGCTGGTTCATGATGAGAAAGCAGAGTGCACCATATATTCACAGAA 386
Oy 252 ThrLeuAlaGlnTyrSerLysGlnMetLysAsnLeuThrMetGluArgGlyAspGln 271
Dh 387 ACCTGGCAGACAGATATTCTTAAGCAATAGACATCTCATGAAAGAGTGACACAG 446
Oy 272 TrpProPheLeuSerGlyLeuGlnTrrPheLysArgArgLysArgAlaValAsnProSer 291
Dh 447 TGGGCCCTTCTCTCTGTAATTAACAGTGGTGAAGAAAGAGAGAGAGATTCATCA 506
Oy 292 ArgGlyIlePheGlnGluMetLysTyrLeuGlnLeuMetIleValAsnAspHisLysThr 311
Dh 507 CGTGTATATTTAAGAAATGAATATTTGAACTTATGATGTGTAATGATCAACAAAGC 566
Oy 312 TyrLysLysHisArgSerSerHisAlaHisThrAsnAsnPheAlaLysSerValAsn 331
Dh 567 TATTAAGAGCATGCGCTTCTTCATGCACATACCAACACTTTTGAAGTCCGTGTCAAC 626
Oy 332 LeuValAspSerIleTyrLysGlnGlnLeuAsnThrArgValAlaLeuValAlaValGlu 351
Dh 627 CTGTGGATTTCTATTATTAAGAGAGCAGCTCAACACCGAGGTTCCTGTGGGTGTAGAG 686
Oy 352 ThrTrrPheLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGlu 371
Dh 687 ACCTGACCTAGAGAGATGAGATTCAGATTCACCCCAACCTGTGCAGATGCTCCAGAG 746
Oy 372 PheSerLysTyrArgGlnArgGlnIleLysGlnHisAlaAspAlaValHisLeuIleSerArg 391
Dh 747 TTCTCAAAATACCGGCGAGCGCATTAAGCAGATGCTGATGCTGTGCACCTCATCTCCGG 806
Oy 392 ValThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyValCysSerArgThr 411
Dh 807 GTGACATTTCACTATATAGAGAGCAGTGTGATTACTTTGAAGGTGCTGTTCGCGACA 866
Oy 412 ArgGlyValGlyValAsnGlyTyrGlyLeuProMetAlaValAlaGlnValLeuSerGln 431
Dh 867 AGAGGAGTGTGCTGAAATGAGTATGCTTCATGACAGTGCAGTGCACAAATATATCCAG 926
Oy 432 SerLeuAlaGlnAsnLeuGlyIleGlnTrrProSerSerArgLysProLysCysAsp 451
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Oy 452 CysThrGluSerTrpGlyGlyCysIleMetGlnGlyThrGlyValSerHisSerArgLys 471
Dh 987 TGCACAAATCTCGGGGTGCTGATCATGAGAGAAACAGGGGTGTCCTCATTTCCGAAA 1046
Oy 472 PheSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGlyGlyAlaCys 491
Dh 1047 TTTTCAAAAGTGCAGCATTTTGGAGTATAGAGACTTTTACAGAGAGAGGTGACCTGC 1106
Oy 492 LeuPheAsnArgProThrLysLeuPheGlnProThrGlyCysGlyAsnGlyTyrValGlu 511
Dh 1107 CTTTTCACAGGCGCAACAGATATTTTGAAGCCCGCAAAATGTGAATGTGATACGTGAA 1166
Oy 512 AlaGlyGlnGlyLysAspCysGlyPheHisValGlnCysTyrGlyLeuCysCysLysLys 531

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1167 GCTGGGGGGGAGTGTGATTTGGTTTTCATTCGTAATGCTATGATATATGCTGTAAGAAA 1226
QY 532 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 551
Db 1227 TGTTCCTCCCTCCAAAGGGGCTCACTGACGACGAGGGCCCTGCTGTAACAAATACCTCAATG 1286
QY 552 LeuPheGlnProAlaGlyTyrGluCysArgAspAlaValaLanGluCysAspIleThrGlu 571
Db 1287 CTTTTCAGCCACGAGGGGTATGAATGCGGGATGCTGTGAACGATGATGATTAATCTANA 1346
QY 572 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAla 591
Db 1347 TATTTACTGGAGACTCTGTGTCAGTCCCAACCAATCTTCATTAACCAAGACGATATGCA 1406
QY 592 CysAsnGlnAsnGlnGlyArgCysTyrAsnGlnGlyCysLysThrArgAspAsnGlnCys 611
Db 1407 TGCATTCAAATCAGAGCGCGCTGCTACATGCGAGTGCAGACCAACCAACCAAGTGT 1466
QY 612 GlnTyrIleTrrGlyThrLysAlaAlaGlySerAspLysPheCysTyrGluLysLeuAsn 631
Db 1467 CAGTACATCTGGGGAACAAGGCTGCAAGGCTGCAACATCTGCTATGAAAAAGCTGAAT 1526
QY 632 ThrGluGlyThrGluLysGlnCysGlyLysAspGlyAspArgTrrIleGlnCysSer 651
Db 1527 ACAGAAAGCAGCTGAGAAAGGAAACTCGGGGAAGATGAGACCGGTGATTCAGTCCAGC 1586
QY 652 LysHisAspValaPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProAlaGly 671
Db 1587 AAACATGATGTGTCTGTGATCTTACTGACCAATCTTACTGACCTCCACGTATTT 1646
QY 672 GlyGlnLeuGlnGlyLysIleIleProIleThrAsnLeuThrArgAlaGly 691
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QY 692 CysSerGlyAlaHisValaLysAspAspThrAspValaGlyTyrValaGlnAspGly 711
Db 1707 TGCATGCTGCCATGTAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1766
QY 712 ThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeu 731
Db 1767 ACCGATGTGGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1826
QY 732 AsnMetSerSerCysProLeuAspSerLysGlyLysValaCysSerGlyHisGlyValaCys 751
Db 1827 AATATGAGCAGCTGTCCACTGATTCAGAGGTAAAGTCTGTGGGCCATGGGGTGTGT 1886
QY 752 SerAsnGlnAlaThrCysIleCysAspPheThrTrrAlaGlyThrAspCysSerIleArg 771
Db 1887 AGTATGAGCAGCCTGATTTGATTTTCACTGGCAGGAGCAGATTTGCAATATCCGG 1946
QY 772 AspProValaArgAsnLeuHisProProLysAspGlnGlyProLysGly 787
Db 1947 GATCCAGTTAGGAACCTTCAACCCCAAGATGAAGACCAAGGAT 1994

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RESULT 3

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US-09-809-617-1
; Sequence 1, Application US/09809617
; Patent No. US20020137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Desher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1

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; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; NAME/KEY: (3)...(2090)
; NAME/KEY: misc_feature
; LOCATION: (1)...(2268)
; OTHER INFORMATION: n = A,T,C or G
US-09-809-617-1

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Alignment Scores:
Pred. No.: 0 Length: 2268
Score: 3621.00 Matches: 654
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 2
Query Match: 79.53% Indels: 0
DB: Gaps: 0

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US-09-634-252a-4 (1-832) x US-09-809-617-1 (1-2268)

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QY 132 LeuAspThrLysAlaArgHisGlnGlnLysHisAsnLysAlaValaHisLeuAlaGlnAla 151
Db 27 CTTGACACAAAGCAAGACACACCAACAAATTAAGGCTGTCCATCTGCGCCAGCA 86
QY 152 SerPheGlnIleGlnAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGly 171
Db 87 AGCTTCAGATTTGAACCTTCGCTCCCAATTCATTTGACCTCACTGACCAATGCT 146
QY 172 LeuLeuSerSerAspTrrValaGluIleHisTyrGluAsnGlyLysProGlnTrrSerLys 191
Db 147 TTGTTCTCTTGATTTATGAGATTCACAGAAATGGGAACACACGATCTAAG 206
QY 192 GlyGlyGlnHisCysTyrTrrHisGlySerIleArgGlyValaLysAspSerLysVala 211
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QY 212 LeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAspThrPheValTrrMetIle 231
Db 267 CTGTCACCTTCGCAATGAGATTCATGCTGATTTGAAGATATACCTTCTGCTATGATTA 326
QY 232 GluProLeuGlnLeuValaHisAspGlyLysSerThrGlyArgProHisIleIleGlnLys 251
Db 327 GAGCAGCTACAGCTGTTTCATGATGAGAAAGACAGAGTGCACATATATCCAGAAA 386
QY 252 ThrLeuAlaGlyGlnTrrSerLysGlnMetLysAsnLeuThrMetGluArgGlyAsnGln 271
Db 387 ACCTTGCAGACAGATTTCTTAAGCAATGAAATCTCACTATGAGAAAGAGGTGACAG 446
QY 272 TrrProPheLeuSerGluLeuGlnTrrLeuLysArgArgLysArgAlaValaLysProSer 291
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QY 292 ArgGlyIlePheGlnGluMetLysTrrLeuGlnLeuMetIleValaAsnAspHisLysThr 311
Db 507 CTTGATATTTTGAAGAAATGAATATTTGGAACCTTATGATTTGATATGATCAACAAAACG 566
QY 312 TyrLysLysHisArgSerSerHisAlaHisThrAsnAsnPheAlaLysSerValValaAsn 331
Db 567 TATAGAGCAGATCGCTTCTTCATGACATACCAACCACTTGGAAAAGTCCGTGGTCAAC 626
QY 332 LeuValaAspSerIleTrrLysGlnGlnLeuAsnThrArgValaValaLeuValaValaGlu 351
Db 627 CTTTGGATTTCTATTATTAAGAGAGAGCTCAACACAGAGGCTTCTGCTGGCTGTAGAG 686
QY 352 ThrTrrPheGlnLysAspGlnIleAspIleThrTrrAsnProValaGlnMetLeuHisGlu 371
Db 687 ACCTGAGCTGAGAAAGATCAGATTGACATCACCAACCAACCTGTCCAGATGCTCATGAG 746
QY 372 PheSerLysTrrArgGlnArgIleLysGlnHisAlaAspAlaValaHisLeuIleSerArg 391
Db 747 TTCTCAAAATACCGGAGCGCATTAAGCAGATGCTGATGCTGACCTCACTCTCGCGG 806

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OY	332	ValThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyValAlcysSerArgThr	411
Db	807	GTCACATTTCACATATAAGAGAAGCAGCTGCAGCTTACTTTGAAGAGTCCTCTTCGCACA	866
OY	412	ArgGlyValGlyValAsnGlnTyrGlyLeuProMetAlaValAlaGlyValLeuSerGln	431
Db	867	AGAGGAGTTGGTGTAATGAGTATGTGCTTCCAAATGGCAGTGGCACAGATATTATTCGACG	926
OY	432	SerLeuAlaGlnAsnLeuGlyTLeuGlnTrpGluProSerSerArgLysProLysCysAsp	451
Db	927	AGCCGTGGCTCAAAACCTTGGAAATCCAAATGGGAACCTTTAGCAGAAAGCCAAATATGTGAC	986
OY	452	CysThrGluSerTrpGlyGlyCysIleMetGluGlnThrGlyValSerHisSerArgLys	471
Db	987	TGCACAGATCCTGGGGTGGCTGCATCATCGAGGAACAGGGGTGTCCCATTCGCAAAA	1044
OY	472	PheSerLysCysSerTLeuGlnTyrArgAspPheLeuGlnArgGlyGlyValAcys	491
Db	1047	TTTTCAAAAGTCGACGATTTTGGAGTATAGAGCTTTTACAGAGAGCAGCTGGACCTCC	1100
OY	492	LeuPheAsnArgProThrLysLeuPheGluTrpThrGlyCysGlyAsnGlyTyrValGlu	511
Db	1107	CTTTTCAACAGGCCCAACAAGCTATTGAGCCCCAGCAGATGTGGAAATGCATACGTGGAA	1166
OY	512	AlaGlyGluGlyCysAspCysGlyPheHisValGlyCysTyrGlyLeuCysCysLysLys	531
Db	1167	GCTGGGGAGAGTGTGATTTGTGCTTTTCATGTGGAATGCTAATGATATGCTGTAAAGAA	1222
OY	532	CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAlaAsnThrSerCys	551
Db	1227	TGTTCCCTCTCCAAACGGGGCTCAGTCAGCGACGCGGCCCTGCTGTACAAATACCTCATGT	1286
OY	552	LeuPheGlnProArgGlyTyrGlyCysArgAspAlaValAsnGlyCysAspTLeuThrGlu	571
Db	1287	CTTTTTCAGCCACGAGGGGTATGAAATGCCGGGATGCTGTGACAGCATGTGATTTACTGCA	1344
OY	572	TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAla	591
Db	1347	TATGTACTGGAGACTCTGTGTCAGTCCACCACCAATCTTCATTAACCAAGCCGATATGCA	1400
OY	592	CysAsnGlnAsnGlnGlyArgCysTyrArgAsnGlyCysLysThrArgAspAsnGlnCys	611
Db	1407	TGCATATCAAAATCAGGGCCCTGCTTACATGGCGAGTGCACAGCCAGCAAGPACAACGAGT	1466
OY	612	GlnTyrIleTrpGlyThrLysAlaAlaGlySerAspLysPheCysTyrGlyLysLeuAsn	631
Db	1467	CAGTACATCTGGGGAAACAAGGCTCAGAGGTCGTGACAAGTTCTGTTATGAAAAGCTGAA	1522
OY	632	ThrGluGlyThrGlyLysGlyAsnCysGlyLysAspGlyAspArgTyrPLeuGlnCysSer	651
Db	1527	ACAGAAAGCCATGTAGAAAGGAAACGCGGAAAGATGTGAAGACCGGTGATTCAGTCAGAC	1586
OY	652	LysHisAspValPheCysGlyPheLeuLeuGlySerAsnLeuThrArgAlaProArgIle	671
Db	1587	AAACATGATGATTTCTGTGATTTCTTACTCTGTACCAATCTTACTACAGCTCCACAGTAT	1640
OY	672	GlyGlnLeuGlnGlyGlnIleIleProThrSerPheTyrHisGlnGlyArgValIleAsp	691
Db	1647	GGTCAACTTCAGGGGAGATCATTTCCACTTCCTTCTACACATCAAGACCCGGGTATTATAC	1706
OY	692	CysSerGlyAlaHisValValLeuAspAspAspThrAspValGlyTyrValGlyLysPgly	711
Db	1707	TGCAGTGGTCCCATGTAGTTTATGATGATATACGATGCGGCTTATGTAGAAATGGA	1766
OY	712	ThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnTLeuGlnAlaLeu	731
Db	1767	ACGCCATGTGGCCGCTCTATGATATGTTTAAATCGGAAGTCCCTATCAAAATTCAAACCTTA	1826
OY	732	AsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValAlcys	751
Db	1827	AATATAGACACACTGTCCATCGATTTCCAAAGGATAAGTCTGTCCGGACCATGGGGTGTCT	1886
OY	752	SerAsnGlnAlaThrCysIleCysAspPheThrTrpAlaGlyTyrAspCysSerTLeuArg	771

```

Db      1887 AGTAATGAAGCCACCTGCATTTGTTGATTTACCTTGGCAGGAGACAGATTGCATGTCCGG 1948
      |||||||
Qy      772 AspProValArgAsnLeuHisProProLysAspGluGlyProLysGly 787
      |||||||
Db      1947 GATCCAGTATTAGGACCTTCACCCCCCAAGATGAAGGCCAACAGGT 1994
      |||||||

RESULT 4
US-09-809-790-3
; Sequence 3, Application US/09809790
; Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Paul O.
; APPLICANT: Bairdour, Nand
; APPLICANT: Delisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2088
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zdincl amino acid degenerate sequence
; NAME/KEY: variation
; LOCATION: (1)...(2088)
; OTHER INFORMATION: n is any nucleotide
; NAME/KEY: misc.feature
; LOCATION: (1)...(2088)
; OTHER INFORMATION: n = A,T,C or G
US-09-809-790-3

Alignment Scores:
Pred. No.: 3,84e-300 Length: 2088
Score: 3007.00 Matches: 528
Percent Similarity: 80.61% Conservative: 0
Best Local Similarity: 80.61% Mismatches: 127
Query Match: 66.04% Indels: 0
DB: 10 Gaps: 0

US-09-634-252A-4 (1-832) x US-09-809-790-3 (1-2088)
Qy      133 AspThrLysAlaIaArgHisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSer 152
      |||||||
Db      28 GAYACNAARCGCMNGMCAYCARGARARCAVAAYAAARGCNGINCAAYTTNGCCARGCMNSN 87
      |||||||
Qy      153 PheGlnIleGluAlaIaPheGlySerLysPheIleLeuAspLeuIleLeuAsnGlyLeu 172
      |||||||
Db      88 TTYCCARAHGARGCMTTYGGMWSNAARPTTYATHTNGAYTYTNATHTYTNAAAYAAAGGAYTN 147
      |||||||
Qy      173 LeuSerSerAspTrpValGluIleHisIyrGlnLysGlyLysProGlnIntYrSerLysGly 192
      |||||||
Db      148 YTNMSNMSNGAYTATGATGARATTCATYAYGARAAYGGNAARCCNCAATTAATWSNAARGN 207
      |||||||
Qy      193 GlyGlnHisCysTrpTrpHisGlySerIleArgGlyValLysAspSerLysValAlaLeu 212
      |||||||
Db      208 GGNARGCAVGTGTATYATACAYAGGMSNNTTHMGNGCNGTNAARGAAYWSMAARGTNGCYTN 267
      |||||||
Qy      213 SerThrCysAsnGlyLeuHisGlyMetPheGlnAspAspThrPheValTyrMetIleGlu 232
      |||||||
Db      268 WSNACMTGYAAYGGNYTTCAYAGNATGTTYGARAYGAYACNTTYGTWTATGATGCAR 327
      |||||||
Qy      223 ProLeuGluLeuValHisAspGluLysSerThrGlnArgProGlnIleIleGlnLysThr 252
      |||||||
Db      328 CCNTTNGARITYNGINCAIGATGARAAARASNACGNGMNGCNCAYATHTATHCARAARACN 387
      |||||||
Qy      253 LeuAlaGlyGlnTrpSerLysGlyMetLysAsnLeuThrMetGluATCGLYAASGlnTrp 272
      |||||||

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Db      388 YTNCGNGNCARTAWNSAARARATGAARAATTNACNATGGAGMGNGCAYCARTGG 447
Oy      273 ProPheLeuSerGluLeuGlnTrpLeuLysArgArgAlaValAsnProSerArg 292
Db      448 CCNTTYTNMSGAVTYTCARTGGTYTNAARMGNCNMGNCNGTNAAYCCNMSNMGN 507
Oy      293 GlyIlePheGluGluMetLysTrpLeuGluMetIleValAsnAspHisLysThrTrp 312
Db      508 GGNATHHTTGGARCATGATGAATTAATYTNNGARTNATGATGNGNAAGCAVCAARACNTAY 567
Oy      313 LysLysHisArgSerSerHisAlaHisThrAsnAsnPheAlaLysSerValValAsnLeu 332
Db      568 AARAAKCAIWMGWSMNSCAYCCNCAACNAAYATTTGCCNAARSNSTNGTNAAYTN 627
Oy      333 ValAspSerIleTrpLysGlnIleLeuAsnThrArgValValLeuValAlaValGluTrp 352
Db      628 GNGAGVNSAATHTAATAAARGARCATYTNAAACNMNGTNGTNTNGTNCNGTNGARCN 687
Oy      353 TrpThrGluLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGluPhe 372
Db      688 TGACACGAAARAARCAATGATGATGATACACNAAYCCNGTNCARATGTTNCAYGARTTY 747
Oy      373 SerLysTrpArgGlnArgIleLysGlnHisAlaAspAlaValHisLeuIleSerArgVal 392
Db      748 WSAARATATMGNCARMGNTHAARCARCAVGCNGATGNGTNCAYTNTATWMSMNGTIN 807
Oy      393 ThrPheHisTrpLysArgSerSerLeuSerTrpPheGlyGlyValLysSerArgThrArg 412
Db      808 ACNTTYCAVTAAYAAARMGWSMNSNTYTNWMSNTATTTGGARNGTNGTNGWSMNGACMGN 867
Oy      413 GlyValGlyValAsnGluTrpGlyLeuProMetAlaValAlaGlnValIleSerGlnSer 432
Db      868 GGNCTGNGTNAAYGARTAGTGGTYTNCNATGGCNGTNCNCARNTNTNWSMCAWMSN 927
Oy      433 LeuAlaGlnAsnLeuGlyIleGlnTrpGluProSerSerArgLysProLysCysAspCys 452
Db      928 YTNCGNCARAAAYTNGSNATHCATGTGGARCCNMSNMNNAARCCNAARTGGAYTGY 987
Oy      453 ThrGluSerTrpGlyLysIleMetGluGluThrGlyLysSerHisSerArgLysPhe 472
Db      988 ACNGARMSNTGGGNGGNGTGAATGATGARGARACNGNGTNGWSMNGAARTTY 1047
Oy      473 SerLysCysSerIleLeuGluTrpArgAspPheGlnArgGlyGlyAlaCysLeu 492
Db      1048 WSAARCTGWSNATHYTNGATGATGATGATTTTNCARMGNGGNGGNGCNGTGYTIN 1107
Oy      493 PheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsnGlyTrpValGluAla 512
Db      1108 TTYAAYMGNCNACNAARTYTTTGGARCCNACNGARCTGCGNAAYGGTAYGTNGARCN 1167
Oy      513 GlyIleGluCysAspCysGlyPheHisValGluCysTrpGlyLeuGlyCysLysLysCys 532
Db      1168 GGNARGARCTGAYTGGTTCAYTCAYTNGARTGYTGGNYTNTGTTGAARARAGY 1227
Oy      533 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAspThrSerCysLeu 552
Db      1228 WSNYTNMSNAAYGGGNCATTTGYSNCAAYGNCNCNTGYTGAATAAACMSNTGYTIN 1287
Oy      553 PheGlnProArgGlyTrpGluCysArgAspAlaValAsnGluCysAspIleThrGluTrp 572
Db      1288 TTYCARCCNMGNGTAYGARTGYGNGAYGCGTNAAYGARTGYGAYATHACNGARAY 1347
Oy      573 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTrpLacys 592
Db      1348 TGYACNGNGAGAWMSGNCARTGYCCNCAAYTNCAVAAARCAAGVGGNTAYGCTGY 1407
Oy      593 AsnGlnAsnGlnGlyArgCysTrpArgAsnGlyGluCysLysThrArgAspAsnGlnCysGln 612
Db      1408 AAYCARAAVCAARGMNGTGYTAAYAGNGARCTGTAARACMNGCAVAYARCTGYCAR 1467
Oy      613 TyrIleTrpGlyThrLysAlaAlaGlySerAspLysPheCysTrpGlyLysLeuAsnThr 632
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Db      1468 TAYATHTGGGNACNAARCGNCGNMSNCAVAAARTTGTGTAYGARARATNNAAYCN 1527
Oy      633 GlnGlyThrGluLysGlyAsnCysGlyLysAspGlyAspArgTrpIleGlnCysSerLys 652
Db      1528 GARGNACNGAARAAAGNAATYGTGCGNARAGVGGNGAVGNTGATHCARFGYWSNAR 1587
Oy      653 HisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGly 672
Db      1588 CAVGAVGTNTTGTGGTNTTYTNTGTCACNAAYTNACMNGMNGCNCNMGNTATHGON 1647
Oy      673 GlnLeuGlnGlyGlnIleLeuProThrSerPheTrpHisGlnGlyArgValIleAspCys 692
Db      1648 CARYTNCARGNGARTRTHATGCCNACMSNTTYYATCAICARGMNGNTNTNTHGAYTGY 1707
Oy      693 SerGlyAlaHisValValLeuAspAspThrAspValGlyTrpValGluAspGlyTrp 712
Db      1708 WMSGGNCACATGNTNTNTNGAYGAYACAGATGNGTNGATNGARCGYGGNACN 1767
Oy      713 ProCysGlyProSerMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsn 732
Db      1768 CCNTGYGNCNMSNATGATGTGTGTGTGAYMGNAARTGYTTCARATHCARGCNTYNAAY 1827
Oy      733 MetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCysSer 752
Db      1828 ATGMSMWSNTGYCCNTTNGATYWSNARGAARAGTMTGWSMNGCAYGNGTNGYWSN 1887
Oy      753 AsnGluAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArgAsp 772
Db      1888 AAYGARCCNACNTGTATHTGTGATYACNTGGCGNCGNCAAYTGYSNATHMGNGAY 1947
Oy      773 ProValArgAsnLeuHisProProLysAspGlnGlyProLysGly 787
Db      1948 CCNCTMGNAAYTTCAYCCNCAARAGATGARCGNCCNAARGN 1992

RESULT 5
US-09-809-617-3
: Sequence 3, Application US/09809617
: Patent No. US20020137178A1
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Balindur, Nand
: APPLICANT: Delsher, Theresa A.
: APPLICANT: Bishop, Paul D.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOG
: FILE REFERENCE: 98-29
: CURRENT APPLICATION NUMBER: US/09/809,617
: PRIOR FILING DATE: 2001-03-15
: PRIOR APPLICATION NUMBER: US/09/351,414
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2088
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: zdin1 amino acid degenerate sequence
: NAME/KEY: variation
: LOCATION: (1)...(2088)
: OTHER INFORMATION: n is any nucleotide
: NAME/KEY: misc_feature
: LOCATION: (1)...(2088)
: OTHER INFORMATION: n = A,T,C or G
US-09-809-617-3

Alignment Scores:
Pred. No.: 3, 84e-300
Score: 3007.00
Percent Similarity: 80.61%
Best Local Similarity: 80.61%
Query Match: 66.04%
DB: 10
Matches: 2088
Conservative: 528
Mismatch: 127
Indels: 0
Gaps: 0
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US-09-634-252a-4 (1-832) x US-09-809-617-3 (1-2088)

QY 133 AsPThrLysAlaArgHisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSer 152
DB 28 GAYACMAARCGMNCNCAVCARCARARARCAVAAARCGNGTNCAYTTTNGCCARCGMNSN 87

QY 153 PheGlnIleGluAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnGlyLeu 172
DB 88 TTYCARATHGARGCNTTGGNMNSNAARTTYATHTNGAYTTNATHYNAAYAAAGVNTN 147

QY 173 LeuSerSerAspTyrValGluIleHisTyrGluAsnGlyLysProGlnTyrSerLysGly 192
DB 148 YTNMSMNSNGAYTYAGTNGARATHCAYAAAGARAAVGGNARCCNCTNTATYMSNARCGN 207

QY 193 GlyGluHisCysTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAlaLeu 212
DB 208 GGNARCACTYTTATYATCAICAGMMSNATHMNGNGTNAARGAWNAAGTNGCNTN 267

QY 213 SerThrCysAsnGlyLeuHisGlyMetPheGluAspAspThrPheValTyrMetIleGlu 232
DB 268 MSNACNTGAYAGGNTNCAYGAGNATGTTGARGAYGACNTTYGNTATATGATHGAR 327

QY 223 ProLeuGluLeuValHisAspGlyLysSerThrGlyArgProHisIleIleGlnLysThr 252
DB 328 CCNTNGARNTNGNCAYGAGARAAARMSNACNGMNCNCAYACATTCARARACN 387

QY 253 LeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMetGluAspGlyAspGlnTyr 272
DB 388 YTNCGNGCNCARNTYWSMAARCARATGARAATYTNACNATGARGMNGGNCATCARCG 447

QY 273 ProPheLeuSerGluLeuGlnTyrPheLysArgArgLysArgAlaValLysProSerArg 292
DB 448 CCNTTYTYMNSNGARNTTCARTGCTYTNAAARMGNCNARMCNGCNGNAACCMNSMNGN 507

QY 293 GlyIlePheGluGluMetLysTyrLeuGluLeuMetIleValAsnAspHisLysThrTyr 312
DB 508 GGNATHTTYGARARATGAATATATYTNATGARTNATGARGNAAYGACATTAARCCNTAY 567

QY 313 LysLysHisArgSerSerHisAlaHisThrAsnAspPheAlaLysSerValValAsnLeu 332
DB 568 AARARARCAVMGMSMNCAYGCNCAYACNAAYATTYGCAARARMSNGTNGTNAAYTN 627

QY 333 ValAspSerIleTyrLysGluGlnLeuAsnThrArgValLysValAlaValGluThr 352
DB 628 GTNCAYSNATHTYAAARGARCARATNAAYACNMNGTNGTNGTNGCNGTNGARACN 687

QY 353 ThrPheGluLysAspGlnIleAspIleThrAsnProValGlnMetLeuHisGluPhe 372
DB 688 TGGACNGARARARGAVCARATGAAVATHACNACNAAYCCNGTNCARATCTYTCAYGARTTY 747

QY 373 SerLysTyrArgGlnArgIleLysGlnHisAlaAspAlaValHisLeuIleSerArgVal 392
DB 748 MSNAARFAYMNCARBMGNATHAARCARAYCCNGAYCCNGTNCAYTTNATYMSMNGCNTN 807

QY 393 ThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyValCysSerArgThrArg 412
DB 808 ACNTTYCACTYAAARMGMSMNSNTYTNASTYTCARGCGNTNTYWSMNGNACNMGN 867

QY 413 GlyValGlyValAsnGluTyrGlyLeuProMetIleValAlaGlnValLeuSerGlnSer 432
DB 868 GGNATNGNGTNAAYTGARTATGAGTNTCCNATGGCNGTNCARNTYTNMSNARASN 927

QY 433 LeuAlaGlnAsnLeuGlyIleGlnTyrPheProSerSerArgLysProLysCysAspLys 452
DB 928 YTNCCNCARAAVYTNNGNATHCARCGGARGCCNMSMNGMAARCAARTGAYTYG 987

QY 453 ThrGluSerTyrPheGlyGlyLysIleMetGluGluThrGlyValSerHisSerArgLysPhe 472
DB 988 ACNARMSNTGGGNGGNTGATATGARGARACNGCNGTMSNCAYWSMNGNAARTTY 1047

QY 473 SerLysCysSerIleLeuGluTyrArgAspPheLeuGlnArgGlyGlyValCysLeu 492
DB 1048 MSNAARCTGYMSNATHYTNGARTATMGNCAYTTTYTNCAARMGNGGNGCNGCNTGYTN 1107

QY 493 PheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrValGluAla 512
DB 1108 TTYAAYMNCNCCNACNAARTYTTTTCARCCMNCNARTRGGMNAAYGNTATGTCARBCN 1167

QY 513 GlyGluGluCysAspCysGlyPheHisValGluCysTyrGlyLeuCysCysLysLysCys 532
DB 1168 GNGCARGARCTGYGATGGNTTCAYGTCNARGTYATYAGGNTYNTGYTGYAARAARPTGY 1227

QY 533 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAspThrSerCysLeu 552
DB 1228 WSNYTNMSNAAYGGNGCCAYTGWSNCAVGCNCCNTGYTAAVAAACWMSMTGYTN 1287

QY 553 PheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyr 572
DB 1288 TTYCARCCMNGNGTATGARTGYGNCAYCCNGTNAAYGARTGYATATTCARCARPAY 1347

QY 573 CysThrGlyAspSerGlyGlnCysProPheAsnLeuHisLysGlnAspGlyTyrAlaCys 592
DB 1348 TGYACNGNGNCAVWSMNGNCARTGYCCNCCNAAVYTNCAVAAARCARAGVAGMTATGCTGY 1407

QY 593 AsnGlnAsnGlnGlyArgCysTyrAsnGlyCysLysThrArgAspAsnGlnCysGln 612
DB 1408 AAYCARAAVCAARGGMGNTGYTAAVAAVGNARCTGYAARACMNGAYAAVCAARTGYCAR 1467

QY 613 TyrIleTyrPheGlyThrLysAlaAlaGlySerAspLysPheCysTyrGluLysLeuAsnThr 632
DB 1468 TATATHTGGGNCNACNAARCGCNGCNGMNSNCAVAAARTTYTGTATGARAARTYTNAAVACN 1527

QY 633 GluGlyThrGluLysGlyAsnCysGlyLysAspGlyAspArgTyrPheIleGlnCysSerLys 652
DB 1528 GARGGNACNGARARARCGNAAVYTGCGNAAARAYGNGAYGKMTGNTGATTCARTGYWSNAAR 1587

QY 653 HisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGly 672
DB 1588 CAYGAYGNTTYTGTGGNTTYTNNTYTNVACMAAYTNACMNGCNCMNGNATTHGCGN 1647

QY 673 GlnLeuGlnGlyGluIleIleProThrSerPheTyrHisGlnGlyArgValIleAspCys 692
DB 1648 CARTNCARCGNGARATHTATTCNACNMSNTTYATYCAVCAARGGMGNTNATHCATYGY 1707

QY 693 SerGlyAlaHisValValLeuAspAspAspThrAspValGlyTyrValGluAspGlyThr 712
DB 1708 WSNCGNCCNCAVGTGNTYTNAGAYGAYACNGAYGTCNGTATGARGAYGAGNACN 1767

QY 713 ProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsn 732
DB 1768 CCNTGYGCGCCMWSNATGATGTGYTNGAYMGNAARCTGYTNCAARATTCARCGCNTNAY 1827

QY 733 MetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCysSer 752
DB 1828 ATGMSNMSNTGCTCCNTYTNATGATWSNAARCGNARAGTNTGWSNCGNCAVGGTNGTNGWSN 1887

QY 753 AsnGluAlaThrCysIleCysAspPheThrTyrPalGlyThrAspCysSerIleArgAsp 772
DB 1888 AAYGARGCNCNACNTGATHTGYATTYACNTNGCGCNGNACNAGATGYWSNATHMGNAY 1947

QY 773 ProValArgAsnLeuHisProProLysAspGluGlyProLysGly 787
DB 1948 CCNGTNGMNAAYTYTNCAVCCNCCNAAARGAYGARGGNCNAAARGN 1992

RESULT 6
US-09-792-200B-17
Sequence 17, Application US/09792200B
Patent No. US20020042368A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Fanslow, William C.
APPLICANT: Poindexter, Kurt
APPLICANT: Cerretti, Douglas P.
APPLICANT: Black, Roy A.
TITLE OF INVENTION: INTECHIN ANTAGONISTS
FILE REFERENCE: 2958-A


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CURRENT APPLICATION NUMBER: US/09/792, 200B
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/184, 865
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 1668
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion Construct
NAME/KEY: CDS
LOCATION: (25)..(1647)
OTHER INFORMATION:
US-09-792-200B-17

Alignment Scores:
Pred. No.: 2,4e-163 Length: 1668
Score: 1680.00 Matches: 288
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 36.90% Indels: 0
DB: Gaps: 0

US-09-634-252a-4 (1-832) x US-09-792-200B-17 (1-1668)
QY 503 ThGluCysGlyAsnGlyTyrValGluAlaGluGluCysAspCysGlyPheHisVal 522
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DB 85 ACTAGTGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 144
QY 523 GluCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCysSerAsp 542
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 145 GAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
QY 543 GlyProCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGlyCysArgAsp 562
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 205 GGGCCCTGCTGTAACATACCTCATGCTCTTTTTCAGCCAGGAGTATGATGCGCGGAT 264
QY 563 AlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyInCysProPro 582
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 265 GCTGTGAACGAGTGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
QY 583 AsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyrAsnGly 602
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 325 AATCTTCTAATGACAGAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 384
QY 603 GluCysLysThrArgAspAsnGlnCysGlnTyrIleThrGlyThrLysAlaAlaGlySer 622
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 385 GAGTGCAGAGGCGCAGACCAACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 444
QY 623 AspLysPheCysTyrGlyLysLeuAsnThrGluGlyThrGluLysGlyAsnGlyLys 642
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 445 GACAAGTCTGCTATGAAAGAGCTGAATACAGAAAGGCACTGAGAAAGGAAACTGCGGAG 504
QY 643 AspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeuLeuLys 662
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 505 GATGAGACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 564
QY 663 ThrAsnLeuThrArgAlaProArgIleGlnLeuGlnGlyAlaIleIleProThrSer 682
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 565 ACCAATCTTACTCGAGCTCCAGCTATGCTCAACTTCAGGGTGAATATCATTCACACTTCC 624
QY 683 PheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValValLeuAspAsp 702
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 623 TTTCTACATCAAGCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 684
QY 703 ThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCysLeuAsp 722
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 685 ACGGATGTGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 744
QY 723 ArgGlyCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGly 742
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DB 745 CGAAGTGCCTACAAATTCACACCCCTAAATATGACGAGTGTCCAGCTGATCCAGGCT 804
QY 743 LysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAspPheThr 762
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 805 AAGTGTGTGCGCCATGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 864
QY 763 TrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProProLysAsp 782
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 865 TGGCGAGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 924
QY 783 GluGlyProLysGlyProSerAlaThrAsn 792
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 925 GAAGGACCCAGAGGCTGTAGTGCACCAAT 954

RESULT 7
US-10-020-733-9
Sequence 9, Application US/10020733
Patent No. US20020161214A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilgenowski, Nathaniel L.
APPLICANT: Fiddie, Carl Johan
TITLE OF INVENTION: NO. US20020161214A1 Human Proteases and Polynucleotides Enco
FILE REFERENCE: LEX-0263-USA
CURRENT APPLICATION NUMBER: US/10/020,733
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: US 60/244, 939
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 3512
TYPE: DNA
ORGANISM: homo sapiens
US-10-020-733-9

Alignment Scores:
Pred. No.: 1,05e-95 Length: 3512
Score: 1029.50 Matches: 266
Percent Similarity: 44.35% Conservative: 115
Best Local Similarity: 30.97% Mismatches: 341
Query Match: 22.61% Indels: 137
DB: Gaps: 31

US-09-634-252a-4 (1-832) x US-10-020-733-9 (1-3512)
QY 4 ProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGlyAlaSerCys 23
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 52 CTTCTTCATATCTCGGAGAGCCCGGAGGCTGAGCGGAGCGTTCGACAGAGGCTGAGCGG 111
QY 24 GlyProGlnArgGlyProAlaGlySerValProAlaSerAlaPro----- 38
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 112 GTGGGAGGCGCGGCGGAGCGCGGCGGCTTCAGACGCGGCTCCACGCGCGGCGAGTGG 171
QY 39 -----AlaArgThrProPro--- 43
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 172 CAGTATGCTGAGGCGGTGAGCGCGGAGCGGCTTAAGCGCGCGCGCGCCACCATGCCAGG 231
QY 4 -----CysArgLeuLeuLeuValLeuLeuLeuLeuLeuProProLeuAlaAlaSer 59
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 232 GCGCGAGCGCGCGCGCGCTGCTGCTGCGGCGTTTGCCTGCGACGCCCTC----- 282.
QY 60 SerArgProArgAlaTrpGlyAlaAlaAlaProSerAlaProHisIleTrpAsnGluThrAla 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 283 ---CGGCGCGG-----CGCGCGCGGAGCGCTGATGGACAAGAGAGAGT 324
QY 80 GluLysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerSer 99
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 325 GAGGAAGC----- 333
QY 100 AsnIleSerTyrSerAsnAlaMetGlnGlyIleThrLeuProSerArgLeuIleTyr 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 334 -----AGCCCAAGCTGAGCATGTATCATCATCTCAGTGG----- 372

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Oy	120	Tyrlleasn	gnaspser	serglsu	serpro	tyrhis	valleu	asprthr	lys	sal	arghis	139	
			
Db	373	-----	-AAGACTT	CAGAAAG	CCCGCTG	-----	-----	-----	-----	-----	-----	393	
Oy	140	glnlysh	isa	snlysa	laval	his	leu	la	gln	la	ser	pheli	159
			
Db	394	-----	-ACAGAA	AACCAT	TCACAT	CAAC	CTCA	AGAG	CTG	CA	GAGGTAA	TGCGTAGG	441
Oy	160	serlysh	pheli	leu	asprleu	lleu	as	na	sn	glnly	leu	ser	179
			
Db	442	CGAA	AACTGAT	CTCG	AGCTTGG	AAGAC	AGATAG	CAACTTTT	TGCTCT	CTTAC	ACACAA	501	
Oy	180	lle	his	tyr	-----	gln	as	ngly	lys	pro	gln	tyr	196
			
Db	502	ACCA	TATTA	TACT	CTCA	AGTGG	TAA	ACCTT	TAAC	CAAC	CA	GGAAT	561
Oy	197	tyr	tyr	his	gln	ser	leu	argly	val	lys	aspr	lys	216
			
Db	562	TTTT	TAAC	CGAC	CGAC	GGTGA	GAGAC	AGAA	CTGTCC	AC	CGCTC	AGCATTTGG	621
Oy	217	gln	leu	his	as	gln	met	pheli	-----	aspr	phr	pheli	235
			
Db	622	GGA	TTAG	AG	AG	CA	TCG	TAT	TAC	CGTGA	GC	AGCA	681
Oy	236	leu	val	his	aspr	gln	lys	ser	thr	gln	arg	pro	255
			
Db	682	-----	-GACAC	CAAG	GGCG	-----	-CAAC	ACCTTA	TTTAC	ACA	-----	711	
Oy	256	gln	tyr	ser	lys	gln	met	lys	-----	as	leu	thr	270
			
Db	712	-----	-TCTGA	ACAT	CTCA	AC	CGCCG	CGCGG	AAATCT	GTGGT	CTG	GCAT	765
Oy	271	-----	-gln	tyr	pro	pheli	ser	gln	leu	gln	tyr	leu	287
			
Db	766	ACCA	CAAG	AG	CA	CTGG	CGT	-----	CTTCA	GT	TTTAC	ACAC	822
Oy	288	val	as	pr	ose	arg	gln	tyr	leu	pheli	gln	leu	307
			
Db	823	ATG	-----	-AAA	AGG	CA	GAATTTAA	ACT	CTCA	GTGA	GTGG	AG	876
Oy	308	aspr	his	tyr	thr	tyr	lys	his	his	arg	ser	his	327
			
Db	877	GAT	TAT	TAG	AG	CTT	CA	GA	AAAT	TC	GA	AA	936
Oy	328	ser	val	val	as	leu	val	aspr	ser	leu	tyr	lys	347
			
Db	937	GAG	AT	CGG	CA	CT	GT	TGAT	AG	CTTTA	CG	CA	993
Oy	348	val	al	val	as	gln	tyr	thr	thr	thr	gln	lys	367
			
Db	994	GTC	GGCT	TGG	AG	AGTGG	AG	CC	AG	CA	ATG	GTGA	1051
Oy	368	met	leu	his	gln	leu	pheli	ser	lys	tyr	arg	gln	385
			
Db	1054	ACCC	CTG	TCG	CTT	CTT	CTC	AGT	TGG	AG	CG	CA	1113
Oy	386	val	his	leu	leu	ser	arg	val	thr	pheli	ser	tyr	405
			
Db	1114	GCCC	AA	TTAA</									

OY	463	GLIthrGlyValSerThrIleSerThrIlePheSerLeuGlySerSerIleLeuGlnIleTyrArgAsp	482
Db	1345	GCACATGGGACCCCTTTCCCAAGTGTTCATAGATGTCACACAGAGGACACTGGACAG	1404
OY	483	PheLeuGlnIArgIleGlyIleAlaCysLeuPheAsnArgPro-----ThrLysLeuPhe	500
Db	1405	TATCTGCAGTCCAGTGGTGGAAATGTGTCTTCACAAATGCGACACACAGCATGTATTGAT	1464
OY	501	GLIurThrGlnCysGlnAsnGlyTyrValGlnIleGlnCysAspCysGlyPhe	520
Db	1465	GGAGCGCCGACGTGTGGAGACGGGTATCTGGAAATGGCGAAGATGTGATGTGGAA	1524
OY	521	HisValGluCysTyrGlyLeuCysCys-----LysLysCysSerLeuSerAsnGlyAla	538
Db	1525	GAAGAGAAATTAACAAACCCCTGCTGCATGCCCTTAATTGTTACCTGTAGGCCGGGGCG	1584
OY	539	HisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgIleTyr	558
Db	1585	GAGTGTGTCTCAGGCTCTCTGCTGCCAC-----CAGTGTAACTGTTGGCTCTCTGGGACC	1638
OY	559	GLuCysArgAspAlaValAsnGlnCysAspIleThrGlnIleTyrCysThrGlyAspSerGly	578
Db	1639	CTGTGCGCGGACAGGCCAGGACAGTGTACTCCCGGAGTTCTGTACGGGACACTCTCC	1698
OY	579	GlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnIleArg	598
Db	1699	CACGTGCCCTTACCAACTTCTACCAATGSGATGTACCCCTGTGAAGGGCGGCGACGGCTAC	1758
OY	599	CysTyrAsnGlnIleCysLysThrArgAspAsnGlnCysGlnIleTyrGlyThrLys	618
Db	1759	TGCTTAAACAGGCAATGTGCTCAGCTACACAGAGACGATCCGACAGCTGTGGGACCCGGA	1818
OY	619	AlaIleArgSerAspLysPheCysTyrGlnLysLeuAsnThrGlnGlyThrGlnLysGly	638
Db	1819	GCCCGACCTGCCCTGACCTCTGCTCGAAGGTAATGTGGACAGAGACACCTTTTGA	1878
OY	639	AsnCysGlyLysAsp---GlyAspArgTyrIleGlnCysSerLysHisAspValPheCys	657
Db	1879	AACGTGTGAAAGACATGAATGTGTAAACACAGAAAGTCAACATGAGAGATCCGAAAGT	1938
OY	658	GlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyLeu	677
Db	1939	GGGAAGATCTGAGCTGACAGACTCTGAGGCCCGGCC-----CTGGAGCTCAAC	1988
OY	678	IleIlePro-----ThrSerPheTyrHisGlnArgValIleAspCysSerGlyAla	695
Db	1987	GGGGGCGCAATTGACACCACTATCATCTGAATGGAGGACAGATCTCACTGGCGGGGACCC	2048
OY	696	HisValValLeu-----AspAspAspThrAspValGlyTyrValGlnAsp	710
Db	2047	CACGTCTACGAGGCTCGAGAGGAGGTGACATGCTGACACCGAGGCTGTGATGACT	2106
OY	711	GlyThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAla	730
Db	2107	GGAACCAAGTGTGGCTTACACCATATTTGCTTTGGGGGCGAGTCCAGAACACTCTCTTC	2166
OY	731	LeuAsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyVal	750
Db	2167	TTTGAACCTGAAGCTGT-----GGGAAGAGTCAATGGCCATGGGCTC	2211
OY	751	CysSerAsnGlnAlaThrCysIleCysAspPheThrTyrAlaGlyThrAspCysSerIle	770
Db	2212	TGTAAACACACACAGAACCTCCACAGTCTGCGCGGGCTGGGCCCGCCCTTCTGCACACA	2271
OY	771	ArgAspProValArgAsnLeuHisProProLysAspGlnGlyProLysGlyProSerAla	790
Db	2272	CCGGGCCACGGGGCAGTATC-----GACACTGGGGCTTATGCCCTGTGAGAGT	2319
OY	791	ThrAsnLeuIleIleGlySerIleAlaGlyAlaIleLeuValAlaIleValLeu	809
Db	2320	GTGGTCTCTGTGTACTGAGATGTTGTGGCCATCTTGGTCTGGCGGCTGCTCATG	2376

RESULT 8


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OY 318 SerHisAlaHisThrAsnAspPheAlaLysSerValAlaAsnLeuValAsnSerIleTyr 337
Db 749 GACACAGAGGACCCCAACAAAGCTCATAGAGATGCCCACTATGTATAGTTTATC 808
OY 338 LysGluGlnLeuAsnThrArgValAlaLeuValAlaValGluThrThrGlnLysAsp 357
Db 809 CGA---TCCCTTGAACTCCGGATGCTCTGCGGCTGGAGTGTGGACCCCGGGAAC 865
OY 358 GlnIleAspIleThrAsnProValGlnMetLeuHisGlnPheSerLysTyrArgGln 377
Db 866 ATGTGTGAAGTTTCAAGAAATCATATGTACCCCTGGCTGCTCTGTCAAGTTGGAGCGC 925
OY 378 ArgIle-----LysGlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHis 395
Db 926 AACCTGCTTCCCAAGATGCATGCATGCACAAAGCCCAATTAATCAAGGAGATGCTCCAC 985
OY 396 TyrLysArgSerSerLeuSerTyrPheGlnLysSer-----ArgThrArgLys 413
Db 986 GGCACACACATCCGGCTGGCCCCCTCATGGCCATGCTGTCTGTACACAGTCTGGAGA 1045
OY 414 ValGlyValAsnGlnLysThrGlnLeuProMetAlaValAlaGlnValLeuSerGlnSerLeu 433
Db 1046 GTCAACATGCACACATCCGAGATGCCATGTGGCTGGCTGCCCAACAGCCCAAGAGATG 1105
OY 434 AlaGlnAsnLeuGlnLysIleGlnTyrGlnProSerSerArgLysProLysCysAspCysThr 453
Db 1106 GCCCACAACCTTGGCATGACCCATGATTCGCAGAT-----TGCCTCTGGCCAGT 1156
OY 454 GluSerThrGlnLysGlnLysIleMet---GluGlnThrGlnLysIleSerHisSerArgLysPhe 472
Db 1157 GCGGCTATGATGGGTGATCATGTGACAGCTGCCACCTGGGACCCCTTCCCAAGTGTTC 1216
OY 473 SerLysCysSerIleLeuGlnLysArgAspPheLeuGlnArgGlnLysGlnLysLeu 492
Db 1217 AATGATGATCAACACAGAGAGACTGCAGATCTGCAGATGAGTGGTGGAAATGTCTCTC 1276
OY 493 PheAsnArgPro-----ThrLysLeuPheGlnProThrGlnLysGlnLysGlnLysVal 510
Db 1277 TCCAACTATGCCAGACACAGAGATGTGTATGAGGCGCGAGAGTGTGGAGGGGTATCTG 1336
OY 511 GlnLysGlnLysGlnLysAspCysGlnPheHisValGlnCysTyrGlnLysCys--- 529
Db 1337 GAAAGATGGGAAAGATGTGATCTGGAGAAAGAGAAATTAACAACCCCTGCTGCAT 1396
OY 530 ---LysLysCysSerLeuSerAsnGlnLysHisCysSerAspGlnProCysCysAsnAsn 548
Db 1397 GCTCTATATGTACCCCTGAGCGCGGCGGAGTGTCTCAAGGCTCTCTCCCTGCCAC--- 1453
OY 549 ThrSerCysLeuPheGlnProArgGlnLysGlnCysArgAspAlaValAsnGlnCysAsp 568
Db 1454 ---CAGTGTAACTGCTTGGCTCTGGGACCCCTGTGCGCGAGGACGACGAGGAGTGTAC 1510
OY 569 IleThrGlnLysCysThrGlnLysAspSerGlnLysGlnCysProProAsnLeuHisLysGlnAsp 588
Db 1511 CTCCTGGAGTTCTGTACGGGCAAGTCTCCCACTCCCTACCAACTTCTACAGATGTGAT 1570
OY 589 GlyTyrAlaCysAsnGlnAsnGlnLysArgCysTyrAsnGlnLysCysLysThrArgAsp 608
Db 1571 GGTACCCCTGTGAGGCGCGGCGGCTACTGTCTCAACAGGATGTGCTCTCACTACACAG 1630
OY 609 AsnGlnCysGlnTyrIleThrGlnLysThrLysAlaIleAspLysAspPheCysTyrGln 628
Db 1631 GAGCAGGTGCGACACTGTGGGACCCGAGCCGACACTGCTGACCTTGTCTGAG 1690
OY 629 LysLeuAsnThrGlnGlnLysGlnLysCysGlnLysAsp---GlnAspArgTyr 647
Db 1691 AAGGTAATGTGGCAGACACACTTGTGAATCTGGAAAGACATGAAATGTGAACAC 1750
OY 648 IleGlnCysSerLysHisAspValPheCysGlnPheLeuLeuCysThrAsnLeuThrArg 667
Db 1751 AGGAAGTCAACATGATGAGATGCGAAGTGTGGGAAGATCTCACTGTACAGACTCTGAGGCC 1810

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OY 668 AlaProArgIleGlnLeuGlnLysIleLeuPro-----ThrSerPheTyrHis 685
Db 1811 CGGCCC-----CTGGAGTCCAAACCGGGTGGCCATGTGACACACTATCATCATG 1858
OY 686 GlnGlyArgValIleAspCysSerGlnLysValHisValLeu-----Asp 700
Db 1859 AATGGAGGACAGATGACAGTGGCGGACCCAGCTTACCGAGGTCCTGAGGAGAGGT 1918
OY 701 AspAspThrAspValGlnLysArgValGlnAspArgLysThrProCysGlnProSerMetCys 720
Db 1919 GACATGCTGACCCAGAGGCTGTGATGACTGGAACCAAGTGTGGCTACACCATTTTGGC 1978
OY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerCysProLeuAspSer 740
Db 1979 TTTAGAGGCGACATGCAGAAACCTCTCTTGAACATGAAAGCGTGT----- 2026
OY 741 LysGlnLysValCysSerGlnHisGlnLysSerAsnGlnAlaThrCysIleCysAsp 760
Db 2027 ---GGGAAAGATGCAATGAGCCATGGGCTGTGTAAACACACAGCAACTGCACATGCCCTG 2083
OY 761 PheThrThrAlaGlnLysThrAspCysSerIleAspAspProValArgAsnLeuHisProPro 780
Db 2084 CCGGCTGGGCCCCGCCCTTCTGCACACACCGGCGGAGGCGGAGTATC----- 2134
OY 781 LysAspGlnGlyProLysGlnProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800
Db 2135 ---GACAGTGGGCTATGCCCTGAGAGTGTGGTCTGTGATCGTGTGAGTGTGTG 2191
OY 801 AlaIleLeuValAlaIleValLeu 809
Db 2192 GCCATCTTGTGCTGGCGGTCTCATG 2218

RESULT 10
US-10-020-733-3
: Sequence 3, Application US/10020733
: Patent NO. US20020161214A1
: GENERAL INFORMATION:
: APPLICANT: Walke, D. Wade
: APPLICANT: Miljanowski, Nathaniel L.
: APPLICANT: Fridde, Carl Johan
: TITLE OR INVENTION: NO. US20020161214A1 Human Proteases and Polynucleotides Enco
: FILE REFERENCE: LEX-0263-USA
: CURRENT APPLICATION NUMBER: US/10/020, 733
: PRIOR FILING DATE: 2001-10-30
: PRIOR APPLICATION NUMBER: US 60/244, 939
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 2757
: TYPE: DNA
: ORGANISM: homo sapiens
US-10-020-733-3

Alignment Scores:
Pred. No.: 1,34e-93 Length: 2757
Score: 1007.50 Matches: 252
Percent Similarity: 45.32% Conservative: 111
Best Local Similarity: 31.46% Mismatches: 325
Query Match: 22.13% Indels: 113
DB: 9 Gaps: 29

US-09-634-252A-4 (1-832) x US-10-020-733-3 (1-2757)
OY 38 ProAlaAlaThrProProCysArgLeuLeuValLeuLeuLeuProProLeuAla 57
Db 4 CCAAGGCGCGCAGCGCGCCGCGCTGTGCTGTGCTGCGCTTGGCCCTGCACGCCCTC--- 60
OY 58 AlaSerArgProArgAlaThrPrpLysAlaAlaAlaProSerAlaProHisThrAsnGln 77
Db 61 -----CGGCGCGCG-----GCGGCGCGGAGACCTCGATGACACAGA 96
OY 78 ThrAlaGlnLysAsnLeuGlnValLeuAlaAspGlnAspAsnThrLeuGlnGlnAsnSer 97

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Db 97 GGAAGTAGGAAGC----- 111
Oy 98 SerSerAsnIleSerTySerAsnAlaMetGlnIleGluIleThrLeuProSerArgLeu 117
Db 112 -----AGCCCAAGCTGCAGCATGACATTCATACCTCACTGC--- 150
Oy 118 IleTyTrIleAsnGlnAspSerGluSerProTyTrhIleValLeuAspThrLysAlaArg 137
Db 151 -----AAGACTTCAGAAAGCCCGTG----- 171
Oy 138 HisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAla 157
Db 172 -----AGAGAAAGACATCCACTCAAGCTGAGCTCAGGGTAATGGCT 213
Oy 158 PheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGlnLysLeuLeuSerSerAspTyr 177
Db 214 GAGGGGCGAGACATGATCTGGACCTGAGAGAAATGACAACTTTTGTCTCTCTAC 273
Oy 178 ValGluIleHisTyT---GluAsnGlyLysProGlnTySer-----LysGlyGlyGlu 194
Db 274 ACAGAAACCATTTACTTCAAGTGTGAACCTCAACACACACACAGCAATTTGGAGAT 333
Oy 195 HisCysTyTrhIleHisGlySerIleArgGlyValLysAspSerLysValAlaLeuSerThr 214
Db 334 CACGCTTTTACACGCGACGCGAGGAGACAGAACTGTCACAGCTCAGCCTCAGCACT 393
Oy 215 CysAsnGlyLeuHisGlyMetPheGlu---AspAspThrPheValTyMetIleGluPro 233
Db 394 TGCCGAGGAATTAAGAGACTGATTAACGTGACGACGACAACTCAGCTCAGTATGAGGCC 453
Oy 234 LeuGluLeuValHisAspGluLysSerThrGlyArgProHisIleIleGlnLysThrLeu 253
Db 454 CTCCTC-----GACAGCAAGGCC-----CAACACCTTATTACAGA----- 489
Oy 254 AlaGlyGlnTySerLysGlnMetLys-----AsnLeuThrMetGluArgGly 269
Db 490 -----TCGAAACATCTCAAGCCGCCGCCGAGAACTGTGCTTGACCACTCC 537
Oy 270 Asp-----GlnTrpProPheLeuSerGluLeuGlnTrPLeuLysArgArgLys 285
Db 538 AAGCCCAACACAGGAGCTGGCT---CTTCAGTTTACACAAACAGACACAGACAGCACT 594
Oy 286 ArgAlaValAsnProSerArgGlyIlePheGlnGlnMetLysTyTrhGluLeuMetIle 305
Db 595 CGCAGAGT-----AAAAGGAAGATTAACTCCATGAAGTATGTGGACTTTTACCCTC 648
Oy 306 ValAsnAspHisLysThrTyLysLysHisArgSerSerHisAlaHisThrAsnAspPhe 325
Db 649 GTGGCTGATTATTTAGAGTTTCAAGAAATCGACAGACACGACGACACCAACACAG 708
Oy 326 AlaLysSerValValAsnLeuValAspSerIleTyTrhLysGlnGlnLeuAsnThrArgVal 345
Db 709 CTCATAGAGATCGCCACATGTTGATAGTTTACCGA---TCCTTGAAACATCCGGATT 765
Oy 346 ValLeuValAlaValGluThrTrpThrGluLysAspGlnIleAspIleThrThrAsnPro 365
Db 766 GCTCTCGGCTTGGAAGTGTGAGCCACGCGGAACATGTGTGAAGTTTCAGAGATCSA 825
Oy 366 ValGlnMetLeuHisGluPheSerLysTyArgGlnArgIle-----LysGlnHisAla 383
Db 826 TATTCTACCTCTGGCTTCTTCAGTTTGAGGCGCAAGCTGTGCGCAAAATACCAT 885
Oy 384 AspAlaValHisLeuLeuSerArgValThrPheHisTyTrhLysArgSerSerLysTyTr 403
Db 886 GACAAGCCCAATTAATACAGGGCATGTCTCCACGCGACACACCAACGCGCTGGCCCC 945
Oy 404 PheGlyGlyValCysSer-----ArgThrArgGlyValGlyValAsnGlyTyTrhGlyLeu 421
Db 946 CTCATGCGCATGTCTGTGTACACTGTGAGAGTCAACAGTCAACAGCACTCCGAGAA 1005
Oy 422 ProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTrp 441
Db 1006 GCCATTGGCTGGCTGCCACCATGGCCACAGATGGGCCAACATTTGGCATGACCAT 1065
Oy 442 GluProSerSerArgLysProLysCysAspCysThrGlnSerTrpGlyGlyLysIleMet 461
Db 1066 GATTCTGCAGAT-----TGCTGCTCGGCCAGTGGCGGTGATGGTGGTGCATATG 1116
Oy 462 ---GlnGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTrp 480
Db 1117 GCAGCTGCACACTGGGCAACCCCTTTCCCAAGTGTTCATATGATGATCAACAGAGAGAGCTG 1176
Oy 481 ArgAspPheLeuGlnArgGlyGlyGlyValLysLeuPheAsnArgPro-----ThrLys 498
Db 1177 GACAGATATGTCAGTACAGGTGCTGGAATGTGTCTTCCAAACATGCGACACAGCATG 1236
Oy 499 LeuPheGluProThrGlnCysGlyAsnGlyTyTrhValGluAlaGlnGlnLysCysAspCys 518
Db 1237 TTGTATGGAGGCCCGAGGTGTGGAGACCGGATCTGGAAGATGGGAGAGATGTGACTGT 1296
Oy 519 GlyPheHisValGluCysTyTrhGlyLysCysCys-----LysLysCysSerLeuSerAsn 536
Db 1297 GGAGAGAGAGAGATGATTAACAAACCCCTGTCGATGCTTATTTGTAACCTTGAGCCG 1356
Oy 537 GlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArg 556
Db 1357 GGGCGGAGTGTGCTCAACGCGCTCCTGCTCCAC-----CAGTGTAACTGTGGTCTCT 1410
Oy 557 GlyTyTrhGlyCysArgAspAlaValAlaAsnGluCysAspIleThrGlnTyTrhGlyAsp 576
Db 1411 GGGAGCCTGTGCGCGAGACAGGCGAGGATGTACCTCCGAGATTTCTGACGGGCAAG 1470
Oy 577 SerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyTrhAlaCysAsnGlnAsnGln 596
Db 1471 TCTCCCACTGCTCCCTACCAACTTCTTACAGATGATGATGATGATGATGATGATGATG 1530
Oy 597 GlyArgCysTyTrhAsnGlyGlnCysLysThrArgAspAsnGlnCysGlnTyTrhGly 616
Db 1531 GCGTACTGTCAACAGGCGATGTGCTGCTCAACAGGAGGAGCGACGACCTGTGGGGA 1590
Oy 617 ThrLysAlaAlaGlySerAspLysPheCysTyTrhGlnLysLeuAsnThrGlnGlyThrGlu 636
Db 1591 CCGGAGACCGGACCTGCGCCCTGACCTGTCTTCAGAAAGGTGATGTGGCAGGACACAC 1650
Oy 637 LysGlyAsnCysGlyLysAsp---GlyAspArgTrpIleGlnCysSerLysHisAspVal 655
Db 1651 TTTTGAAACTGTGGAAAGACATGATGTCGACACAGAGAGTGCACATGAGAGATGGC 1710
Oy 656 PheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGlnLeuGln 675
Db 1711 AAGTGTGGGAAGATCCAGTGTCAAGAGCTTGAGGCCCGGCC-----CTGGAG 1758
Oy 676 GlyGluIleLeuPro-----ThrSerPheTyTrhHisGlnGlyArgValIleAspCysSer 693
Db 1759 TCCAAACCGGCGCCCATTTGACACCACTATATCTCATGATAGGAGGACAGATTCAGTGG 1818
Oy 694 GlyAlaHisValValLeu-----AspAspAspThrAspValGlyTyTrhVal 708
Db 1819 GCGACCCACGCTGACGAGGCTGTGAGAGAGAGGTGACATGTGCGACCCAGGCTGTGG 1878
Oy 709 GluAspGlyThrProCysGlyProSerMetMetCysLysAspArgGlyCysLysGlnIle 728
Db 1879 ATGACTGGAAACCAAGTGTGCTCAACCATATTTTGTGAGGGGCAAGTGCAGAGAAC 1938
Oy 729 GlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHis 748
Db 1939 TCCCTTTTGAACCTGAAGCTGT-----GGAAAGAAAGTGCATGGCCAT 1993
Oy 749 GlyValCysSerAsnGluAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCys 768
Db 1984 GGGGTGTGTAAACACACAGAACTGCGACATGCTGCCGCGGCTGGCGCCGCTCTGCG 2043
Oy 769 SerIleArgAspProValArgAsnLeuHisTrpGluAspGlnGlyProLysGlyPro 788
Db 2044 AACACACCGGCGCCAGCGGGGAGTATC-----GACAGTGGGCGCATATGCCCT 2091
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Oy 254 AlaGlyGlnTyrSerLysGlnMetLys-----AsnLeuThrMetGluArgGly 269
 Db 490 -----TCTGACATCTCAAGCCCGCCCGGAACCTGGTTCAGACACTCC 537
 Oy 270 Asp-----GlnTrpProPheLeuSerGluLeuGlnTrpLeuArgGlyLys 285
 Db 538 AACCCACACACAGGAGCTGGCT---CTTCACATTACACACAGCACAAGAACCCACT 594
 Oy 286 ArgAlaValAsnProSerArgGlyIlePheGluGluMetLysTyrLeuGluMetLys 305
 Db 595 CCGAGAGATG-----AAAGGGAAGATTAACTCCATGATGATGGAGCTTACCTC 648
 Oy 306 ValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAlaHisSerHisAsnPro 325
 Db 649 GTGCTGATATTATTAGAGTTTCAGAAAGATCGACAGAACCCAGCACCACCAACACAAAG 708
 Oy 326 AlaLysSerValAlaAsnLeuValAspSerLysTyrLysGluGlnLeuAsnThrArgVal 345
 Db 709 CTCATAGAGATCGCCACATGTTGATTAAGTTTACCAG---TCCTTGAACATCCGGATT 765
 Oy 346 ValLeuValAlaValGluThrTrpThrGluLysAspGlnIleAspIleThrAsnPro 365
 Db 766 GCCTCTGCTGGCTTGCAGAGTGTGACCCAGCCAGACATGTGTGAAGTTTCAGAGAAATCCA 825
 Oy 366 ValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIle-----LysGlnHisAla 383
 Db 826 TATTCTACCCCTGCTGCTCTTCTCAGTTGGAGCGGCAAGCTGTGCCCGAAGATACCAT 885
 Oy 384 AspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSerLeuSerTyr 403
 Db 886 GACACACCCCAATTAAATACAGGGCATGTCTCTCCACGGCACACCATCGGCTGGCCCCC 945
 Oy 404 PheGlyGlyValLysSer-----ArgThrArgGlyValAlaGlnGluTyrGlyLeu 421
 Db 946 CTCATGGCAGATGCTCTGTGTACAGCTGAGACATGCAATGATGCAACACTCCAGAAAT 1005
 Oy 422 PrometalAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTrp 441
 Db 1006 GCCATTGGCTGGCTGGCCACCATGCGCCACAGATGGCCACACTTGGCATATACCAT 1065
 Oy 442 GluProSerSerArgLysProLysCysAspCysTrpGlnSerTyrGlyLysIleMet 461
 Db 1066 GATTCTGCAGAT-----TGCTGCTGGCCAGCATGGCGGTGATGGGTGCATCATG 1116
 Oy 462 ---GluThrGlyValSerHisSerArgLysPheSerLysCysSerLysLeuGluTyr 480
 Db 1117 GCAGCTGCCACTGGGACCCCTTCCCAAGTGTTCATGATGCACAGAGAGGAGCTG 1176
 Oy 481 ArgAspPheLeuGlnArgGlyGlyLysLysLeuPheAsnArgPro-----ThrLys 498
 Db 1177 GACAGGTTCGTCACTCAAGTGTGTGAAATGTGTCTCCACATGCCAGACACCGAGATG 1236
 Oy 499 LeuPheGluProThrGluGlyLysGlnGlyValAlaGluAlaGlyGluGlnCysAspCys 518
 Db 1237 TTGTATGGAGGGCGGAGGTGTGGAAACGGTATCTGGAAGATGGGAAGAGTGTACTGT 1296
 Oy 519 GlyPheHisValGluCysTyrGlyLysCysCys-----LysLysCysSerLeuSerAsn 536
 Db 1297 GGAGAAGAAGAGAGATGTAAACACCCCTGCTGCAATGCCCTTAATTGTAACCTTGAGGCCG 1356
 Oy 537 GlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArg 556
 Db 1357 GGGGGGGAAGTGTCTACGGCTCTGCTGCCAC-----CAGTGTAACTGTTGGCTCCT 1410
 Oy 557 GlyTyrGluCysArgAspAlaValAlaGlnCysAspIleThrGluTyrCysThrGlyAsp 576
 Db 1411 GGGACCCCTTGGCGGAGCAGGCGCAGGCGAGTGTGACCTCCGAGTTCGTGACGGGCAAG 1470
 Oy 577 SerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGln 596
 Db 1471 TGTCCCACTGGCCCTACCAACTTCTACAGATGATGATGATACCCCTGTGAGGCGGCGCAG 1530

Oy 597 GlyArgCysTyrAsnGlyGlnCysLysThrArgAspAsnGlnCysGlnTyrIleTrpGly 616
 Db 1531 GCGTACTGCTACACAGGCGATGTGCTCACTACAGAGACAGTGTGCGACAGCTGTGGGA 1590
 Oy 617 ThrLysAlaAlaGlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGlu 636
 Db 1591 CCCGAGCCCGAGCTGGCCCTGACCTCTGCTTCGTAAGAGTGAATGTGGCAGGAACACAC 1650
 Oy 637 LysGlyAsnCysGlyLysAsp---GlyAspArgTrpIleGlnCysSerLysHisAspVal 655
 Db 1651 TTGGAACTGTGTGAAGAGCATGAATGTGTGAACACAGGAAGTGCACATCGAGATGGCGG 1710
 Oy 656 PheCysGlyPheLeuLeuMetCysThrAsnLeuThrArgAlaProArgIleGlyLeuGln 675
 Db 1711 AAGTGTGGGAAGATCCAGTGTGACAGCTCTGAGGCCCGGCC-----CTGGAG 1758
 Oy 676 GlyGluIleLeuPro-----ThrSerPheTyrHisGlnGlyArgValIleAspSer 693
 Db 1759 TCCACCGCGGTGCCATTGTACACCACTATCATGATGATGGAGGACATCCAGTCCGG 1818
 Oy 694 GlyAlaHisValValLeu-----AspAspAspThrAspValGlyTyrVal 708
 Db 1819 GGCACCCAGCTTACCGAGGTCTCTGAGAGGAGGTGACATGTGTGACCCAGGCTGTG 1878
 Oy 709 GluAspGlyThrProCysGlyProSerMetCysLeuAspArgLysCysLeuGlnIle 728
 Db 1879 ATGACTGGAACCAAGTGTGCTACAAACCATATTGCTTTGAGGGGCAAGTGCACGAACACC 1938
 Oy 729 GlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlnHis 748
 Db 1939 TCCCTTTTGAACCTGAAGCTGT-----GGGAAGAAGTCAATGCCCAT 1983
 Oy 749 GlyValCysSerAsnGluAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCys 768
 Db 1984 GGGGTCTGTAAACAAACAGAACGTGCGCACTGCGCGGGGCGGCCCTTCTGCG 2043
 Oy 769 SerIleArgAspProValArgAsnLeuHisProProLysAspGluGlyProLysGlyPro 788
 Db 2044 AACACACCGGCGCACGGGCGCAGTATC-----GACAGTGGGCTTATGCCCT 2091
 Oy 789 SerAlaThrAsnLeuIleIleGlySerIleAlaGlyAlaIleLeuValAlaAlaIleVal 808
 Db 2092 GAGAGTGTGGCTGTGTGTAAGTGTGAGTGTGTGTCGCATCTTGTGTGCGCGCTC 2151
 Oy 809 Leu 809
 Db 2152 Arg 2154

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